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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 15:52:02 ; Search time 312 Seconds

(without alignments)
8046.402 Million cell updates/sec

Title: US-09-884-814-2

Perfect score: 930
Sequence: 1 atcgctgggtcgaagccac.....ccgagagctccctctga 930

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N Genesec 19jun03:*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	930	100.0	930	20	AAZ19968
2	930	100.0	930	21	AAZ50624
3	930	100.0	1024	25	ABZ83750
4	930	100.0	1105	20	AAZ99434
5	930	100.0	1105	21	AAZ29323
6	930	100.0	1105	22	AAZ14819
7	930	100.0	1105	22	AAZ02388
8	930	100.0	1643	24	AAZ94928

9	928.4	99.8	930	20	AAZ99435	UCP2 Nucleotide se
10	928.4	99.8	930	24	ABK86151	CDNA encoding huma
11	928.4	99.8	1596	20	AAV82381	Full length human
12	928.4	99.8	1596	21	AAA99716	Mouse body weight-
13	928.4	99.8	1596	21	AAA52254	Human uncoupling p
14	928.4	99.8	1612	19	AAV44595	Human respiration
15	928.4	99.8	1682	21	AAZ29244	Human mitochondria
16	928.4	99.8	1888	20	AAZ99436	UCP2 nucleotide se
17	928.4	99.8	1888	20	ABK84483	Human CDNA differe
18	898.4	96.6	1255	19	AAV05078	Human C5 gene CDNA
19	893.6	96.1	1255	17	AAZ13981	Human body weight
20	880.4	94.7	960	22	AAZ37933	Hybrid hUCP2 DNA.
21	762	81.9	1575	24	ABK3772	Rat sequence diffe
22	618	66.5	1205	19	AAV09077	Mouse C5 gene full
23	618	66.5	1205	19	AAV08360	Full length mouse
24	618	66.5	1205	21	AAV89715	Mouse body weight-
25	618	66.5	1205	21	AAA52253	Mouse uncoupling p
26	614.8	54.7	1205	17	AAZ13980	Brown fat uncoupli
27	508.8	54.7	512	24	ABK38976	CDNA encoding lung
28	508.8	54.7	512	25	ACA11305	Human lung adenoca
29	508.8	54.7	512	25	ACA02481	Lung cancer therap
30	474	51.0	939	22	AAZ19969	Human uncoupling p
31	474	51.0	939	22	AAH18849	Human UCP3 CDNA.
32	474	51.0	1175	21	AAZ29245	Human mitochondria
33	474	51.0	1231	19	AAV72690	Human uncoupling p
34	474	51.0	1231	24	ABO72999	Human uncoupling p
35	473.4	50.9	1204	19	AAV84307	Mouse uncoupling p
36	473.4	50.9	1658	19	AAV54602	Human uncoupling p
37	472.4	50.8	1193	20	AAZ46055	Human uncoupling p
38	472.4	50.8	1193	21	AAZ46055	CDNA encoding a hu
39	472.4	50.8	1193	22	AAZ08530	Human uncoupling p
40	472.4	50.8	1193	22	AAZ08530	Human mitochondria
41	472.4	50.8	1220	19	AAV71710	Human uncoupling p
42	471.8	50.7	2782	20	AAZ07060	Human uncoupling p
43	471.8	50.7	2782	20	AAV71227	CDNA encoding a mu
44	471.8	50.7	2782	21	AAZ90318	CDNA encoding multi
45	471.8	50.7	2782	22	AAZ09318	Mouse uncoupling p

ALIGNMENTS

RESULT 1	AAZ19968	standard; CDNA; 930 BP.
ID	AAZ19968	
AC	AAZ19968:	
XX		
AC	21-DEC-1999	(first entry)
XX		
DT		
XX		
DE		Human uncoupling protein 2 CDNA.
XX		
KW	Uncoupling protein 2; UCP2; human; obesity; diabetes; diagnosis;	
KW	gene therapy; ss.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Variation	replace(164,T)
FT		/tag= a
XX		
PN	NO9946905-A1.	
XX		
PD	30-SEP-1999.	
XX		
PF	23-MAR-1999;	99WO-US06317.
XX		
PR	23-MAR-1998;	98US-0078972.
XX		
FA	(MUSC-) MUSC POUND RES DEV.	
XX		
PI	Garvey WT, Argyropoulos G;	
XX		

DR MPI: 1999-591072/50.
P-PSDB; AA131903.

XX Use of uncoupling protein 2 or 3 as markers for identifying subjects
XX at risk of developing obesity or diabetes -

PS Claim 3; Page 101-102; 112pp; English.

XX This nucleotide sequence represents human uncoupling protein 2
CC (UCP2) cDNA, which codes for a 309-amino acid protein (see
CC AA131903). UCP2 genomic DNA is provided in AA131967. The invention
CC relates to the discovery that the presence of single nucleotide
CC polymorphisms correlates with the development of obesity and/or
CC type II diabetes mellitus. In UCP2, a C164T polymorphism results
CC in substitution of a valine residue for alanine at position 55 of
CC the encoded UCP2 protein. Methods are provided for identifying a
CC subject at risk of developing obesity and/or diabetes by detection
CC of the polymorphism in the UCP2 nucleic acid or amino acid
CC sequence. 3 Further polymorphisms, in the UCP3 gene (see AA19969),
CC are also correlated with obesity and diabetes. UCP2 and UCP3
CC nucleic acids can also be used for gene therapy, for restoring
CC normal function to a gene encoding a gene product involved in
CC obesity and/or diabetes, and for producing transgenic animals.

XX Sequence 930 BP; 185 A; 286 C; 255 G; 204 T; 0 other;

Query Match 100.0%; Score 930; DB 20; Length 930;
Best Local Similarity 100.0%; Pred. No. 3,6e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTGGGTTCAAGCCACAGATGCGCCCTCTGCACTGGAATTTCTGGGGCT 60
DB 1 AAGTTGGGTTCAAGCCACAGATGCGCCCTCTGCACTGGAATTTCTGGGGCT 60
QY 61 GGCACAGCTGCTGATGCAATCTCACTCTCTCTGATCTGCTAAAGTCCG 120
DB 61 GGCACAGCTGCTGATGCAATCTCACTCTCTCTGATCTGCTAAAGTCCG 120
QY 121 TTACAGATCCAGAGAAAGTCAAGGGGCTAGGGGCTTACAGCAGCCGCAATCCG 180
DB 121 TTACAGATCCAGAGAAAGTCAAGGGGCTAGGGGCTTACAGCAGCCGCAATCCG 180
QY 181 GGTGTGATGAGGACCATTTCTGACATGCTGCTAGTGAAGGCCCCGAAAGCTCTCAAT 240
DB 181 GGTGTGATGAGGACCATTTCTGACATGCTGCTAGTGAAGGCCCCGAAAGCTCTCAAT 240
QY 241 GGGCTGTGTCGCGGCTGAGGCGCAATGAGCTTTGCTTGTCCGATCGGCTGTAT 300
DB 241 GGGCTGTGTCGCGGCTGAGGCGCAATGAGCTTTGCTTGTCCGATCGGCTGTAT 300
QY 301 GATTCTGTCAACAGTTCTACACCAAGGAGCTCTGAGCATGTCACATTTGGGAGCCGCTC 360
DB 301 GATTCTGTCAACAGTTCTACACCAAGGAGCTCTGAGCATGTCACATTTGGGAGCCGCTC 360
QY 361 CTAGCAGGACGACACCAAGGTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CTAGCAGGACGACACCAAGGTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AAGTCCGATTCAGAGCTGAGGCGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 AAGTCCGATTCAGAGCTGAGGCGGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 AATGCTTACAAAGCCATTGCGGAGAGAGGTTCCGAGGCTCTGGAAGGACCTCT 540
DB 481 AATGCTTACAAAGCCATTGCGGAGAGAGGTTCCGAGGCTCTGGAAGGACCTCT 540
QY 541 CCCAATGTTGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 CCCAATGTTGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 AAGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 AAGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

QY 661 GCCTTGGGAGCAGGCTTCTGACACTGATGCTGCTCCCTGTAGAGTGTCAAGAG 720
DB 661 GCCTTGGGAGCAGGCTTCTGACACTGATGCTGCTCCCTGTAGAGTGTCAAGAG 720
QY 721 AGATACATGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 AGATACATGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 CTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 CTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 841 GGTTCCTGGAAGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 GGTTCCTGGAAGCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 GCTTGCACCTTCCGAGAGGCTCCCTCTGGA 930
DB 901 GCTTGCACCTTCCGAGAGGCTCCCTCTGGA 930

RESULT 2
AA250624
ID AA250624 standard; cDNA; 930 BP.

AC AA250624;
XX
DT 23-MAY-2000 (first entry)

DE Tulare human uncoupling protein-2 cDNA.

KW Human uncoupling protein-2; UCP2; body weight disorder; screening assay;
KW obesity; underweight disorder; anorectic; anabolic; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..930
FT /tag= a
FT /product= "Human uncoupling protein-2"

PN WO200006087-A2.

PD 10-FEB-2000.

PR 29-JUL-1999; 99WO-US17246.

PR 29-JUL-1998; 98US-0124293.

PA (TULARE) TULARIK INC.

PI Chen J, Amaral MC;

DR MPI: 2000-195157/17.

DR P-PSDB; AA145002.

PT Novel recombinant nucleic acids encoding uncoupling protein-2 with
PT specific alanine and threonine residues, useful for treating body
PT weight disorders e.g. obesity -

PS Claim 8; Page 40; 40pp; English.

XX The present sequence encodes a novel human uncoupling protein-2 (UCP2)
CC used for treatment of body weight disorders. UCP2 gene is used in
CC screening assays to identify modulators of UCP2 biological activity, or
CC as pharmaceutical agents to treat body weight disorders, such as obesity
CC and underweight disorders. This is also used to make antisense and
CC triplex-forming nucleic acids that can inhibit UCP2 gene expression upon
CC administration. Modulators of UCP2 gene expression can be identified by
CC contacting a cell comprising UCP2 promoter operably linked to a reporter
CC gene and a test compound; and detecting the level of reporter gene
CC expression.

XX Sequence 930 BP; 185 A; 286 C; 255 G; 204 T; 0 other;

Query Match 100.0%; Score 930; DB 21; Length 930;
Best Local Similarity 100.0%; Pred. No. 3, 7e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTTGGATTCAAGGCCACAGATGTGCCCTACTGTGCACCTGTGAAGTTCTTGGGGCT 60
   |||||
DB 1 ATGGTTGGATTCAAGGCCACAGATGTGCCCTACTGTGCACCTGTGAAGTTCTTGGGGCT 60
QY 61 GGCACAGCTGCTCGATCGCAGATCTCATACCTTTCTCTGGAATCTGCTAAAGTCCG 120
   |||||
DB 61 GGCACAGCTGCTCGATCGCAGATCTCATACCTTTCTCTGGAATCTGCTAAAGTCCG 120
QY 121 TTACAGATCCAAAGGAAAGTAGGGGGCCAGTGCAGCTACAGCAGAGCCCAAGTACCG 180
   |||||
DB 121 TTACAGATCCAAAGGAAAGTAGGGGGCCAGTGCAGCTACAGCAGAGCCCAAGTACCG 180
QY 181 GGTGTGATGGGACCACTTGTGACCATGTGCGTACTGAGGGCCCCGAAAGCTTACAT 240
   |||||
DB 181 GGTGTGATGGGACCACTTGTGACCATGTGCGTACTGAGGGCCCCGAAAGCTTACAT 240
QY 241 GGGCTGTGCTGGCGGCTGAGGCGCAAAATGAGCTTGTGCTGTGCCGATGGCTGTAT 300
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DB 241 GGGCTGTGCTGGCGGCTGAGGCGCAAAATGAGCTTGTGCTGTGCCGATGGCTGTAT 300
QY 301 GATTCTGTAAACAGTTCTTACACCAAGGCTCTGAGCATGCGAGATTGGAGCGGCTC 360
   |||||
DB 301 GATTCTGTAAACAGTTCTTACACCAAGGCTCTGAGCATGCGAGATTGGAGCGGCTC 360
QY 361 CTGACGAGGACCAACCAAGTGCCTGTGCTGTGCTGTGCGCCAGCCCAAGATGTGTA 420
   |||||
DB 361 CTGACGAGGACCAACCAAGTGCCTGTGCTGTGCTGTGCGCCAGCCCAAGATGTGTA 420
QY 421 AAGTCCGATTCGAAGCTCAGGCGCGGCTGAGGTGTGCGAGTACCAAGACCGTCT 480
   |||||
DB 421 AAGTCCGATTCGAAGCTCAGGCGCGGCTGAGGTGTGCGAGTACCAAGACCGTCT 480
QY 481 AATGCTTACAAAGCACTTGTCCGAGAGAGAGGCTTCCGGGCTTCTGAAAAGGACCTCT 540
   |||||
DB 481 AATGCTTACAAAGCACTTGTCCGAGAGAGAGGCTTCCGGGCTTCTGAAAAGGACCTCT 540
QY 541 CCCAATGTGCTGTGATGCACTTGTGCACTGTGCTGAGTGTGAGTGAACCTATGACCTATC 600
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DB 541 CCCAATGTGCTGTGATGCACTTGTGCACTGTGCTGAGTGTGAGTGAACCTATGACCTATC 600
QY 601 AAGGATGCCCTCTCTGAAGACCACTCATGACAGATGACCTCCCTTGCACCTTCACTTCT 660
   |||||
DB 601 AAGGATGCCCTCTCTGAAGACCACTCATGACAGATGACCTCCCTTGCACCTTCACTTCT 660
QY 661 GCGTTTGGGGGAGGCTTGTGCACTGTGCACTGTGCTGAGTGTGAGTGTGAGTGAAGAG 720
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DB 661 GCGTTTGGGGGAGGCTTGTGCACTGTGCACTGTGCTGAGTGTGAGTGTGAGTGAAGAG 720
QY 721 AGATACATGAACCTGTGCTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTG 780
   |||||
DB 721 AGATACATGAACCTGTGCTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTG 780
QY 781 CTCGAGAAGAGAGGAGGCGGCGGAGCTTCTTCAAAAGGTTCAATGCGCTTCTTCTCGGCTG 840
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DB 781 CTCGAGAAGAGAGGAGGCGGCGGAGCTTCTTCAAAAGGTTCAATGCGCTTCTTCTCGGCTG 840
QY 841 GGTTCCTGGAACGTGTGATGTGTGCTCACTTATGAGCAGCTGAAAGAGCCCTTATGGCT 900
   |||||
DB 841 GGTTCCTGGAACGTGTGATGTGTGCTCACTTATGAGCAGCTGAAAGAGCCCTTATGGCT 900
QY 901 GCGTGAATCTCCGAGAGAGGCTCCCTTTCTTA 930
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DB 901 GCGTGAATCTCCGAGAGAGGCTCCCTTTCTTA 930

```

RESULT 3

AB283760
ID AB283760 standard, cDNA, 1024 BP.

XX AB283760;

AC 14-MAY-2003 (first entry)

DE Toxicologically relevant human nucleotide sequence #919.

KW Toxicologically relevant gene; toxicological response; gene; ss.

OS Homo sapiens.

PN WO2003016500-A2.

PD 27-FEB-2003.

PF 16-AUG-2002; 2002MO-US26514.

PR 16-AUG-2001; 2001US-313080P.

PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kler LD, Schmeisler K;

PI Alen P;

DR WPI; 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening

PT of drugs, comprises comparing the expression profile of one or more

PS human toxic response genes to a reference gene expression profile

XX indicative of toxicity -

XX Claim 1; Page 284; 455pp; English.

The present invention describes a method (M1) for determining a
toxicological response to an agent, which comprises comparing the
expression profile of one or more human toxic response genes to a
reference gene expression profile indicative of toxicity, and so
determining the presence of a toxic response to the agent. Also
described: (1) an array comprising one or more polynucleotides selected
from the genes corresponding to the partial sequences given in AB282842
to AB284764, or their fragments of at least 20 nucleotides, or
homologues; and (2) determining if a gene putatively identified to be a
toxic response gene plays a role on toxic response pathways by
determining the expression profile of the gene after exposure of cells
or a human subject to a known toxic pharmaceutical or industrial agent,
comprising: (a) exposing cells to an agent or isolating cells from a
human subject who was exposed to an agent; (b) obtaining the test gene
expression profile for a putatively identified toxic response gene after
exposure to a known toxic pharmaceutical or industrial agent; and
(c) comparing the test profile to the expression profile of a gene with
a similar function or comparing the test profile to the expression
profile of that gene after exposure to other known toxic compounds. The
methods are useful for predicting and determining toxicological responses
on a cellular, organ or system level. The arrays comprising the human
genes are useful for toxicological screening of drugs, pharmaceutical
compounds and chemicals.

SO Sequence 1024 BP; 200 A; 314 C; 274 G; 236 T; 0 other;

Query Match 100.0%; Score 930; DB 25; Length 1024;
Best Local Similarity 100.0%; Pred. No. 3, 7e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGTTGGATTCAAGGCCACAGATGTGCCCTACTGTGCACCTGTGAAGTTCTTGGGGCT 60
   |||||
DB 89 ATGGTTGGATTCAAGGCCACAGATGTGCCCTACTGTGCACCTGTGAAGTTCTTGGGGCT 148
QY 61 GGCACAGCTGCTGTGATGCAAGATCTCATACCTTTCTCTGATATGTGTAAGTCCGG 120
   |||||
DB 149 GGCACAGCTGCTGTGATGCAAGATCTCATACCTTTCTCTGATATGTGTAAGTCCGG 208

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QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCGCAGTACCGC 180
DB 209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCGCAGTACCGC 268
QY 181 GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCCGAAAGCTCTACAT 240
DB 269 GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCCGAAAGCTCTACAT 328
QY 241 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGACATCGGCTGTAT 300
DB 329 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGACATCGGCTGTAT 388
QY 301 GATTCGTCAAAAGTCTTACACCAAGGGCTCTGAGCATGCCAGCATTTGGAGCCCGCTTC 360
DB 389 GATTCGTCAAAAGTCTTACACCAAGGGCTCTGAGCATGCCAGCATTTGGAGCCCGCTTC 448
QY 361 CTAGCAGGACAGACAGAGTGGCCCTGGCTGTGGCTGTGGCCAGCCAGCATTTGTGTA 420
DB 449 CTAGCAGGACAGACAGAGTGGCCCTGGCTGTGGCTGTGGCCAGCCAGCATTTGTGTA 508
QY 421 AAGGTCGATTCCAAGCTCAGGCCCCGGCTGGAGTGTGGAGATACCAAGCACCGTC 480
DB 509 AAGGTCGATTCCAAGCTCAGGCCCCGGCTGGAGTGTGGAGATACCAAGCACCGTC 568
QY 481 AATGGCTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGGCCCTGTGAAAGGACCTCT 540
DB 569 AATGGCTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGGCCCTGTGAAAGGACCTCT 628
QY 541 CCCAATGTTGCTGTATGCCATGTCTCACTGTGTCTGAGCTGTGACTATGACTCATC 600
DB 629 CCCAATGTTGCTGTATGCCATGTCTCACTGTGTCTGAGCTGTGACTATGACTCATC 688
QY 601 AAGGATGCCCCCTCTTAAGCCAACTCTACATGACATGACCTCCCTCCCACTCACTCTC 660
DB 689 AAGGATGCCCCCTCTTAAGCCAACTCTACATGACATGACCTCCCTCCCACTCACTCTC 748
QY 661 GCCTTTGGGGCAGGCTTCTGACACACTGTCTCCCTCCCTGTGAGAGTGTCAAGACG 720
DB 749 GCCTTTGGGGCAGGCTTCTGACACACTGTCTCCCTCCCTGTGAGAGTGTCAAGACG 808
QY 721 AGATATCATGAACTCTGCCCCCTGGGCGAGTACAGTACGCTGGCCACTGTGCCCTTACATG 780
DB 809 AGATATCATGAACTCTGCCCCCTGGGCGAGTACAGTACGCTGGCCACTGTGCCCTTACATG 868
QY 781 CTCGAGAGAGAGAGGAGCCCGAGCCCTTCTACAAAGGTTCAATGCCCTCTTCTCCGCTTG 840
DB 869 CTCGAGAGAGAGAGGAGCCCGAGCCCTTCTACAAAGGTTCAATGCCCTCTTCTCCGCTTG 928
QY 841 GGTTCCTGGAACGTGTGTATGTTGTCACCTATGAGCAGCTGAAACGAGCCCTCATGTGCT 900
DB 929 GGTTCCTGGAACGTGTGTATGTTGTCACCTATGAGCAGCTGAAACGAGCCCTCATGTGCT 988
QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
DB 989 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 1018

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RESULT 4

AXX9434 ID AAX9434 standard; DNA; 1105 BP.

AXX9434 AC AAX9434.

DT 19-OCT-1999 (first entry)

DE UCP2 Nucleotide sequence.

XX uncoupling protein; nucleotide; mitochondria; diabetes;

KM brown adipose tissue; wild type; obesity; thermo-regulation; ds.

OS Homo sapiens.

XX PN MO9337812-A1.

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XX 29-JUL-1999.
PD 21-JAN-1999; 99MO-US01198.
PF 21-JAN-1999; 99MO-US01198.
XX 23-JAN-1998; 98US-0012218.
FR (ORCH-) ORCHID BIOCOMPUTER INC.
PA Violijk LP;
XX WPI: 1999-469144/39.
XX P-PSDB; AAY28351.
DR A novel single nucleotide polymorphism of the uncoupling protein 2
PT gene, useful for diagnosis, prognosis and treatment of obesity
XX Disclosure; Fig 2; 68pp; English.
XX This is the nucleotide sequence of uncoupling protein-2 (UCP-2) as
CC reported by Boss et al, FEBS Lett 408, 39-42, 1997.
CC Identifying a UCP2 polymorphism, especially Val55 (thymine at
CC nucleotide 164), can be used to diagnose obesity, non-insulin dependent
CC diabetes mellitus and other UCP2 related diseases. Wild-type UCP2
CC generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2
CC related diseases include atherosclerosis, hyperinsulinemia, chronic
CC inflammation, thermogenesis, apoptosis and cachexia.
XX Sequence 1105 BP; 205 A; 345 C; 287 G; 268 T; 0 other;
SQ

```

Query Match 100.0%; Score 930; DB 20; Length 1105;
Best Local Similarity 100.0%; Pred. No. 3.8e-239;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATGTTGGGTTCAAGGACCAAGTGTGCCCCCTACTGACATGTAAAGTTCTTGGGCT 60
DB 89 ATGTTGGGTTCAAGGACCAAGTGTGCCCCCTACTGACATGTAAAGTTCTTGGGCT 148
QY 61 GGCACACCTGCTGATCGAGATCTATCATTCTCTGTGATACCTGTAAGTCCGG 120
DB 149 GGCACACCTGCTGATCGAGATCTATCATTCTCTGTGATACCTGTAAGTCCGG 208
QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCGCAGTACCGC 180
DB 209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCCGCAGTACCGC 268
QY 181 GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCCGAAAGCTCTACAT 240
DB 269 GGTGTGATGGGACCACTTCTGACCATGGTGGTACTGAGGGCCCCGAAAGCTCTACAT 328
QY 241 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGACATCGGCTGTAT 300
DB 329 GGGCTGTGGCGGCTGACAGCCCAATGAGCTTTGCTCTGTCCGACATCGGCTGTAT 388
QY 301 GATTCGTCAAAAGTCTTACACCAAGGGCTCTGAGCATGCCAGCATTTGGAGCCCGCTTC 360
DB 389 GATTCGTCAAAAGTCTTACACCAAGGGCTCTGAGCATGCCAGCATTTGGAGCCCGCTTC 448
QY 361 CTAGCAGGACAGACAGAGTGGCCCTGGCTGTGGCTGTGGCCAGCCAGCATTTGTGTA 420
DB 449 CTAGCAGGACAGACAGAGTGGCCCTGGCTGTGGCTGTGGCCAGCCAGCATTTGTGTA 508
QY 421 AAGGTCGATTCCAAGCTCAGGCCCCGGCTGGAGTGTGGAGATACCAAGCACCGTC 480
DB 509 AAGGTCGATTCCAAGCTCAGGCCCCGGCTGGAGTGTGGAGATACCAAGCACCGTC 568
QY 481 AATGGCTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGGCCCTGTGAAAGGACCTCT 540
DB 569 AATGGCTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGGCCCTGTGAAAGGACCTCT 628
QY 541 CCCAATGTTGCTGTATGCCATGTCTCACTGTGTCTGAGCTGTGACTATGACTCATC 600
DB 629 CCCAATGTTGCTGTATGCCATGTCTCACTGTGTCTGAGCTGTGACTATGACTCATC 688

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QY 841 GGTTCCTGGAACGTGTGATGTTGTGACCTATGAGAGAGCTGAAGAGCCCTCATGGCT 900
 DB 929 GGTTCCTGGAACGTGTGATGTTGTGACCTATGAGAGAGCTGAAGAGCCCTCATGGCT 988
 QY 901 GCCTGCACCTTCCCGAGAGGCTCCCTTCTGA 930
 DB 989 GCCTGCACCTTCCCGAGAGGCTCCCTTCTGA 1018
 RESULT 6
 AAS14819
 ID AAS14819 standard; cDNA; 1105 BP.
 XX
 AC AAS14819;
 XX
 DT 13-DEC-2001 (first entry)
 XX
 DE Human cDNA encoding partial UCP-2 protein.
 XX
 KW Human; Uncoupling protein; UCP-2; ss; transgenic plant; fuel metabolism;
 KW antibacterial; bacterial infection; environmental stress; food.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 74..1018
 FT /*tag= a
 FT /product= "UCP-2"
 FT /partial
 FT /note= "No start codon"
 XX
 PN WO200175131-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10236.
 XX
 PR 31-MAR-2000; 2000US-193533P.
 XX
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Berry-Lowe SL, Newell MK;
 XX
 DR WPI; 2001-626442/72.
 DR P-PSDB; AAI09077.
 XX
 XX Plants expressing heterologous cell-wall uncoupling protein, have
 PT altered metabolism, resistance to infection and stress sensitivity -
 XX
 PS Disclosure; Page 58-59; 72pp; English.
 CC The invention relates to a transgenic plant expressing a cell-wall UCP
 CC (uncoupling protein) encoded by a heterologous gene. The
 CC heterologous UCP, when expressed in the plant cell wall, plasma
 CC membrane or chloroplast regulates the fuel metabolism of the plant.
 CC Regulating expression or activity of UCP is used to control fuel
 CC metabolism, especially reducing UCP expression produces nutritionally
 CC improved plants and protects against infection e.g. bacterial, while
 CC decreasing expression improves sensitivity to light and cold. Altering
 CC UCP activity can improve crop productivity and durability towards
 CC environmental stress, and it eliminates time-consuming and expensive
 CC maintenance and repeated application of chemicals. The present
 CC sequence encodes human UCP-2 and is used as the heterologous UCP in the
 CC method of the invention.
 CC
 SQ Sequence 1105 BP; 205 A; 345 C; 287 G; 268 T; 0 other;
 XX
 XX
 Query Match 100.0%; Score 930; DB 22; Length 1105;
 Best Local Similarity 100.0%; Pred.No.3.8e-239;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGTGGGTTCAAGGCAACAGATGTGCCCCCTACTGCGCACTGTGAAGTTTCTTGGAGCT 60
 XX

DB 89 ATGGTGGGTTCAAGGCAACAGATGTGCCCCCTACTGCGCACTGTGAAGTTTCTTGGAGCT 148
 QY 61 GGCACAGCTGCTGCATCGAGATCTCATACCTTCTCTGGATAGCTAAAGTCCG 120
 DB 149 GGCACAGCTGCTGCATCGAGATCTCATACCTTCTCTGGATAGCTAAAGTCCG 208
 QY 121 TTACAGATCCAGAGGAAAGTCAAGGAGCCATGCGGCTCAACGCCAGCCCAATACCGC 180
 DB 209 TTACAGATCCAGAGGAAAGTCAAGGAGCCATGCGGCTCAACGCCAGCCCAATACCGC 268
 QY 181 GGTGTGATGGGACACCATTTGACCATGAGTGCAGTGAAGAGGAGCCCGAAGCTCTCAAT 240
 DB 269 GGTGTGATGGGACACCATTTGACCATGAGTGCAGTGAAGAGGAGCCCGAAGCTCTCAAT 328
 QY 241 GGGCTGTGTGCGGCTGCAAGCCCAATGAGCTTGTCTGTGCGATCGGCTGTAT 300
 DB 329 GGGCTGTGTGCGGCTGCAAGCCCAATGAGCTTGTCTGTGCGATCGGCTGTAT 388
 QY 301 GATTCTGTCAACAGTTCTACACCAAGGCTCTGACATGACAGATGGAGCGCGCTC 360
 DB 389 GATTCTGTCAACAGTTCTACACCAAGGCTCTGACATGACAGATGGAGCGCGCTC 448
 QY 361 CTACAGAGCAGACACACAGGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 449 CTACAGAGCAGACACACAGGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 508
 QY 421 AAGGTCCGATTTCCAGCTCAGGCTCGGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGT 480
 DB 509 AAGGTCCGATTTCCAGCTCAGGCTCGGCTGTGAGTGTGTGTGTGTGTGTGTGTGTGT 568
 QY 481 AATGCTTACAGACCATTTGCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 DB 569 AATGCTTACAGACCATTTGCTGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 628
 QY 541 CCCAATGTGCTGT 600
 DB 629 CCCAATGTGCTGT 688
 QY 601 AAGGATGCGCTCTGGAAGCCCAACCTCATGACAGATGACCTCCCTTGCACCTTCACTTCT 660
 DB 689 AAGGATGCGCTCTGGAAGCCCAACCTCATGACAGATGACCTCCCTTGCACCTTCACTTCT 748
 QY 661 GCTTTTGGGAGGCTTTCTGACCACTGTATGCTTCCCTGTATAGTGTGTCAAGAG 720
 DB 749 GCTTTTGGGAGGCTTTCTGACCACTGTATGCTTCCCTGTATAGTGTGTGTCAAGAG 808
 QY 721 AGATACATGAACCTGTGCTGCGGCTGAGTACAGTACGCTGACCTGTGCTTACCATG 780
 DB 809 AGATACATGAACCTGTGCTGCGGCTGAGTACAGTACGCTGACCTGTGCTTACCATG 868
 QY 781 CTCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 869 CTCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 928
 QY 841 GGTTCCTGGAACGTGTGATGTTGTGACCTATGAGAGAGCTGAAGAGCCCTCATGGCT 900
 DB 929 GGTTCCTGGAACGTGTGATGTTGTGACCTATGAGAGAGCTGAAGAGCCCTCATGGCT 988
 QY 901 GCCTGCACCTTCCCGAGAGGCTCCCTTCTGA 930
 DB 989 GCCTGCACCTTCCCGAGAGGCTCCCTTCTGA 1018
 RESULT 7
 AAD02388
 ID AAD02388 standard; cDNA; 1105 BP.
 XX
 AC AAD02388;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human uncoupling protein, UCP-2 cDNA.
 XX

KW Human; uncoupling protein; UCP-2; cancer; brain; renal; antiviral;
 KW antibacterial; antifungal; cytostatic; immunosuppressive; scleroderma;
 KW antiarthritic; dermatologic; UCP inhibitor; therapy; antineumatic;
 KW rheumatoid arthritis; leukaemia; tumour; autoimmune disease; SLE;
 KW systemic lupus erythematosus; celiac disease; infectious disease;
 KW pemphigus vulgaris; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 89..1018
 FT CDS /tag= a
 FT /product= "Human UCP-2 protein"
 FT
 XX WO200078941-A2.
 XX
 XX 28-DEC-2000.
 XX
 XX 22-JUN-2000; 2000MO-US17245.
 XX
 XX 23-JUN-1999; 99US-0140574.
 XX
 XX (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX
 XX Newell MK.
 XX
 XX WPI; 2001.102716/11.
 XX P-PSDB; AAY72342.
 XX
 XX Inhibiting plasma membrane uncoupling protein expression in tumor cells
 XX and rapidly dividing bacterial cells, for treating cancer and
 XX infectious diseases -
 XX
 XX Disclosure; Page 104; 106pp; English.
 XX
 XX The present sequence is a cDNA encoding human Uncoupling Protein,
 XX UCP-2. The present invention relates to a method for inhibiting the
 XX expression of plasma membrane uncoupling protein (UCP) in a cell by a
 XX plasma membrane UCP inhibitor. UCP is expressed on lysosomal membranes
 XX and plasma membranes of rapidly dividing cells, but absent in growth
 XX arrested or chemotherapy resistant cells. This method is useful in the
 XX inhibition of plasma membrane UCP expression in tumor cells,
 XX lymphocytes, pancreatic beta cells, rapidly dividing bacterial cells
 XX or B cells. UCP inhibitor is useful in the prevention and treatment of
 XX infectious disease, rheumatoid arthritis, scleroderma and cancers such
 XX as brain cancer, leukaemia, renal cancer, and tumours. The UCP activator
 XX is useful in the treatment of autoimmune diseases such as systemic
 XX lupus erythematosus (SLE), celiac disease and pemphigus vulgaris. UCP
 XX is also useful for inducing cellular division in nerve cells.
 XX
 XX Sequence 1105 BP; 205 A; 345 C; 287 G; 268 T; 0 other;
 XX
 XX Query Match 100.0%; Score 930; DB 22; Length 1105;
 XX Best Local Similarity 100.0%; Pred. No. 3.8e-239;
 XX Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 ATGCTGGGTTCAAGGCGACAGATGCCCCCTACTGCACTGTGAAGTTCTTGGGCT 60
 DB 89 ATGCTGGGTTCAAGGCGACAGATGCCCCCTACTGCACTGTGAAGTTCTTGGGCT 148
 QY 61 GGCACAGCTGCTGCATCGAGATCTGACCTTCCCTGATCTGTAAGTCCGG 120
 DB 149 GGCACAGCTGCTGCATCGAGATCTGACCTTCCCTGATCTGTAAGTCCGG 208
 QY 121 TTACAGATCCAAAGAGAAAGTCAGGGGCGAGTCCGCGCTACAGCCAGCCGCAATCCGC 180
 DB 209 TTACAGATCCAAAGAGAAAGTCAGGGGCGAGTCCGCGCTACAGCCAGCCGCAATCCGC 268
 QY 181 GGTGTGATGGGCAACATTCATGACATGTCGATGAGGGGCGCGGAGGCTTCAAT 240
 DB 269 GGTGTGATGGGCAACATTCATGACATGTCGATGAGGGGCGCGGAGGCTTCAAT 328
 QY 241 GGGCTGTTGGCGGCTGACAGCGCAATGAGCTTTGCTCTGTCGATCGAGCTGTAT 300

DB 329 GGGCTGTTGGCGGCTGACAGCGCAATGAGCTTTGCTGTCGATCGAGCTGTAT 388
 QY 301 GATTGTCAAAAGATTCTACACCAAGGAGCTGTAGCATGACAGATTTGGAGCGGCTC 360
 DB 389 GATTGTCAAAAGATTCTACACCAAGGAGCTGTAGCATGACAGATTTGGAGCGGCTC 448
 QY 361 CTAGCAGCAGACACACAGATGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 449 CTAGCAGCAGACACACAGATGCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 508
 QY 421 AAGTCCGATTCCAGCTCAGGCGCGGAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 DB 509 AAGTCCGATTCCAGCTCAGGCGCGGAGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 568
 QY 481 AATGCTTACAGACATTGCGGAGAGGAAAGGTTCCGGAGCTCTGTGAAAGGAGCTCT 540
 DB 569 AATGCTTACAGACATTGCGGAGAGGAAAGGTTCCGGAGCTCTGTGAAAGGAGCTCT 628
 QY 541 CCCAATGTTGCTGTATATGACATTGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 DB 629 CCCAATGTTGCTGTATATGACATTGTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 688
 QY 601 AAGGATGCTCTGTAAGGCAACCTCATGACAGATGACCTCCCTTGCACCTTCACTTCT 660
 DB 689 AAGGATGCTCTGTAAGGCAACCTCATGACAGATGACCTCCCTTGCACCTTCACTTCT 748
 QY 661 GCTTTGGGCGAGGCTTCTGCACTGTCACTGTCTCCCTGTGTAAGATGTGTCAAGCG 720
 DB 749 GCTTTGGGCGAGGCTTCTGCACTGTCACTGTCTCCCTGTGTAAGATGTGTCAAGCG 808
 QY 721 AGATTCATGAACTCTGCTGAGGCGAGTACAGTACGCTGAGCTGTGCTTGTACAGATG 780
 DB 809 AGATTCATGAACTCTGCTGAGGCGAGTACAGTACGCTGAGCTGTGCTTGTACAGATG 868
 QY 781 CTCACAGAGAGGAGGCGCGGAGCTTCTTCAAAAGGTTCAATGCTCTTCTCTCGCTTG 840
 DB 869 CTCACAGAGAGGAGGCGCGGAGCTTCTTCAAAAGGTTCAATGCTCTTCTCTCGCTTG 928
 QY 841 GGTTCCTGGAAGGT 900
 DB 929 GGTTCCTGGAAGGT 988
 QY 901 GCCTGCACTTCCGAGAGGCTCTCTTGTGA 930
 DB 989 GCCTGCACTTCCGAGAGGCTCTCTTGTGA 1018
 XX
 XX RESULT 8
 XX ID AAS94928 standard; DNA; 1643 BP.
 XX AC AAS94928;
 XX DT 14-FEB-2002 (first entry)
 XX
 XX Human DNA sequence #183 expressed during foam cell differentiation.
 XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;
 XX cardiovascular disorder; coronary artery disease; gene therapy; ds.
 XX Homo sapiens.
 XX OS Homo sapiens.
 XX WO200177389-A2.
 XX
 XX 18-OCT-2001.
 XX PD
 XX 04-APR-2001; 2001MO-US11128.
 XX PF
 XX 05-APR-2000; 2000MO-US1106P.
 XX PR
 XX (INCYTE GENOMICS INC.
 XX PA

PI Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;
 PI Tai J;
 XX WPI: 2002-010925/01.
 DR
 XX Composition useful for diagnosis of conditions, disorders or diseases
 PT associated with atherosclerosis, comprises several polynucleotides that
 PT are differentially expressed in foam cell development -
 XX
 PS Claim 1: Page 238; 315pp; English.
 XX
 CC The present invention relates to the isolation of human polynucleotide
 CC sequences that are differentially expressed during foam cell
 CC differentiation. The polynucleotide sequences of the invention or a
 CC composition comprising these polynucleotides are useful as a high
 CC throughput method for detecting altered expression of one or more
 CC polynucleotides in a sample. The polynucleotides can be used in the
 CC diagnosis of disorders associated with foam cell development such as
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
 CC coronary artery disease. The polynucleotide sequences can also be used
 CC as PCR primers and probes. The polynucleotides of the invention are also
 CC useful in gene therapy. AAS94746-AAS95021 represent the human
 CC polynucleotide sequences of the invention which are differentially
 CC expressed during foam cell differentiation.
 CC
 XX
 SQ Sequence 1643 BP, 311 A; 533 C; 402 G; 397 T; 0 other;

Query Match 100.0%; Score 930; DB 24; Length 1643;
 Best Local Similarity 100.0%; Pred. No. 4,4e-239;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTGGTGGTTAAAGCCACAGATGCGCCCTACTGCTGAGTTCCTTGGGGCT 60
 DB 373 AAGTGGTGGTTAAAGCCACAGATGCGCCCTACTGCTGAGTTCCTTGGGGCT 432
 QY 61 GGCACAGCTGCTGATGACAGATCTCATCACTTCTCTGATGATGTAAGTCCG 120
 DB 433 GGCACAGCTGCTGATGACAGATCTCATCACTTCTCTGATGATGTAAGTCCG 492
 QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTCCGCTTAAGCCAGGCCAGTACCG 180
 DB 493 TTACAGATCCAGAGAAAGTCAAGGGCCAGTCCGCTTAAGCCAGGCCAGTACCG 552
 QY 181 GGTGATGAGGACCACTTCTGACCAATGTCCTACTGAGGGCCGCCAGGCTTACAT 240
 DB 553 GGTGATGAGGACCACTTCTGACCAATGTCCTACTGAGGGCCGCCAGGCTTACAT 612
 QY 241 GGGCTGTTCCGGGCTGACAGGCCAATGACTTTCCTCTGTCGGATGAGCTGAT 300
 DB 613 GGGCTGTTCCGGGCTGACAGGCCAATGACTTTCCTCTGTCGGATGAGCTGAT 672
 QY 301 GATTCTGTCAACAGTCTTACACCAAGGGCTGAGCATGACAGATTGGAGCGGCTC 360
 DB 673 GATTCTGTCAACAGTCTTACACCAAGGGCTGAGCATGACAGATTGGAGCGGCTC 732
 QY 361 CTAGCAGCAGCAGCAGAGTGCCTGCTGTGCTGTGAGCCAGCCAGGATGTGTA 420
 DB 733 CTAGCAGCAGCAGCAGAGTGCCTGCTGTGCTGTGAGCCAGCCAGGATGTGTA 792
 QY 421 AAGTCCGATTCAGACTCAGGCGCGGCTGAGAGTGTGAGATCAAGACAGCTC 480
 DB 793 AAGTCCGATTCAGACTCAGGCGCGGCTGAGAGTGTGAGATCAAGACAGCTC 852
 QY 481 AATGCTTACAGACATGCTGCGCAGAGAAAGGCTTCGGGGCTTGGAAAGGACCTT 540
 DB 853 AATGCTTACAGACATGCTGCGCAGAGAAAGGCTTCGGGGCTTGGAAAGGACCTT 912
 QY 541 CCAATGTTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 913 CCAATGTTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972
 QY 601 AAGATGCTCTCTGAAAGCACTCATGACAGATGACCTCTTGCACCTCACTTCT 660

DB 973 AAGATGCTCTCTGAAAGCACTCATGACAGATGACCTCTCTGACCTCACTTCT 1032
 QY 661 GCTTTGGGAGAGGCTTCTGACACTGATGATGATGATGATGATGATGATGATGAT 720
 DB 1033 GCTTTGGGAGAGGCTTCTGACACTGATGATGATGATGATGATGATGATGATGAT 1092
 QY 721 AGATACATGAACTCTGCTGCTGAGCAGTACAGTACAGTACAGTACAGTACAGT 780
 DB 1093 AGATACATGAACTCTGCTGCTGAGCAGTACAGTACAGTACAGTACAGTACAGT 1152
 QY 781 CTCAGAGAGAGGAGGAGGCTCTCTCAAGGCTTATGAGGCTCTCTCTCTCTCTCT 840
 DB 1153 CTCAGAGAGAGGAGGAGGCTCTCTCAAGGCTTATGAGGCTCTCTCTCTCTCTCT 1212
 QY 841 GGTTCCTGAAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 1213 GGTTCCTGAAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
 QY 901 GCTTGACCTTCCGAGAGGCTCCCTCTCTGA 930
 DB 1273 GCTTGACCTTCCGAGAGGCTCCCTCTCTGA 1302

RESULT 9
 AAX99435
 ID AAX99435 standard; DNA; 930 BP.
 AC AAX99435;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 XX

DE UCP2 Nucleotide sequence (Fleury variant).

KM uncoupling protein; nucleotide; mitochondria; diabetes;
 KM brown adipose tissue; wild type; obesity; thermo-regulation; ds.

OS Homo sapiens.

PN W09937812-A1.

PD 29-JUL-1999.

PF 21-JAN-1999; 99WO-US01198.

PR 23-JAN-1998; 98US-0012218.

PA (ORCH-1) ORCHID BIOCOMPUTER INC.

PI Vrolijk LP;

DR WPI: 1999-469144/39.

DR P-PSDB; AAY28352.

PT A novel single nucleotide polymorphism of the uncoupling protein 2

XX gene, useful for diagnosis, prognosis and treatment of obesity

XX disclosure; Fig 2; 68pp; English.

XX This is the nucleotide sequence of uncoupling protein-2 (UCP-2) as

XX reported by Fleury et al, Nature genetics 1997.

XX CC identifying a UCP2 polymorphism, especially Val15 (thymine at

XX CC nucleotide 164), can be used to diagnose obesity, non-insulin dependent

XX CC diabetes mellitus and other UCP2 related diseases. Wild-type UCP2

XX CC generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2

XX CC related diseases include atherosclerosis, hyperinsulinemia, chronic

XX CC inflammation, thermogenesis, apoptosis and cachexia.

SQ Sequence 930 BP; 185 A; 285 C; 255 G; 205 T; 0 other;

Query Match 99.8%; Score 928.4; DB 20; Length 930;
 Best Local Similarity 99.8%; Pred. No. 9.7e-239;
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGTTGGCTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
DB 1 ATGGTTGGCTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
QY 61 GGCACAGCTGCTGCACTGCAATCTCAATCACTTCTTCTGGAATACGTCTAAAGTCCGG 120
DB 61 GGCACAGCTGCTGCACTGCAATCTCAATCACTTCTTCTGGAATACGTCTAAAGTCCGG 120
QY 121 TTACAGATCCCAAGGAGAAAGTCAAGGGCCAGTGCAGGCTTACAGCCAGCCAGTACCGC 180
DB 121 TTACAGATCCCAAGGAGAAAGTCAAGGGCCAGTGCAGGCTTACAGCCAGCCAGTACCGC 180
QY 181 GGTGTGATGGGCAACCATTTGTACCATGTGTGCTACTGAGGGCCCGAAGCCTTACAAAT 240
DB 181 GGTGTGATGGGCAACCATTTGTACCATGTGTGCTACTGAGGGCCCGAAGCCTTACAAAT 240
QY 241 GGGCTGGTTGCCGCTGAGAGCCCAATGATGACTTGTGCTCTGTCCGATCGGCTGTAT 300
DB 241 GGGCTGGTTGCCGCTGAGAGCCCAATGATGACTTGTGCTCTGTCCGATCGGCTGTAT 300
QY 301 GATTCTGTCAAAACAGTTCTACACAAAGGCTGTGAGCATGCCAGATTGGAGCCGCTC 360
DB 301 GATTCTGTCAAAACAGTTCTACACAAAGGCTGTGAGCATGCCAGATTGGAGCCGCTC 360
QY 361 CTAGCAGGCAAGCAACAGTGCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 420
DB 361 CTAGCAGGCAAGCAACAGTGCCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 420
QY 421 AAGGTCGATTCGAAGCTCAGGCTCCGAGGCTGAGAGTGTGCTGAGATACCAAGACCGCTC 480
DB 421 AAGGTCGATTCGAAGCTCAGGCTCCGAGGCTGAGAGTGTGCTGAGATACCAAGACCGCTC 480
QY 481 AATGCTCAACAAGCCATTGCTCCGAGAGGAGGTTCCGAGGCTCTGGAAGAGGACCTCT 540
DB 481 AATGCTCAACAAGCCATTGCTCCGAGAGGAGGTTCCGAGGCTCTGGAAGAGGACCTCT 540
QY 541 CCCAATGTTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 CCCAATGTTCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 601 AAGGATGCTCTCTGAAAGCAACCTCATGACATGATGATGATGATGATGATGATGATGATG 660
DB 601 AAGGATGCTCTCTGAAAGCAACCTCATGACATGATGATGATGATGATGATGATGATGATG 660
QY 661 GCGTTTGGGCGAGGCTTGTGACCACTGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 GCGTTTGGGCGAGGCTTGTGACCACTGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 AGATACATGAATCTGCTGAGGCAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 780
DB 721 AGATACATGAATCTGCTGAGGCAAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 780
QY 781 CTCCAGAGAGGAGGCGCCGAGGCTTCTCAAAAGGCTTATGCTGCTGCTGCTGCTGCTGCTG 840
DB 781 CTCCAGAGAGGAGGCGCCGAGGCTTCTCAAAAGGCTTATGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 GGTTCCTGAAAGTGTGATGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 900
DB 841 GGTTCCTGAAAGTGTGATGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 GCTTGCACTTCCGAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 GCTTGCACTTCCGAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 901 GCTTGCACTTCCGAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 901 GCTTGCACTTCCGAGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960

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RESULT 10

ABK86151

ID ABK86151 standard; cDNA; 930 BP.

XX AC ABK86151;

XX 26-AUG-2002 (first entry)

XX

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DE cDNA encoding human uncoupling protein UCP-2.
XX Human; uncoupling protein; UCP-2; stroke; ischaemia; epilepsy;
KW neurological disorder; neuronal injury; Parkinson's disease;
KW Huntington's disease; inherited ataxia; motor neuron disease;
KW Alzheimer's disease; traumatic brain injury; bradykinin;
KW serotonin; histamine; arachidonic acid; gene; chromosome 11; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 1..930
FT /tag=a
FT /product="Uncoupling protein UCP-2"
XX MO200236829-A2.
XX 10-MAY-2002.
XX 01-NOV-2001; 2001WO-US45744.
XX 01-NOV-2000; 2000US-244946P.
XX (AGT-) AGY THERAPEUTICS INC.
XX Gonzalez-Zulueta M, Shamloo M, McFarland KC, Chin D, Wieloch T;
XX Melcher T;
XX MPI; 2002-490012/52.
XX P-PSDB; AAU98901.
XX DR
XX PT Diagnosing occurrence of stroke or assessing a patient's susceptibility
XX PT to stroke, by detecting in a patient sample an elevated level of
XX PT uncoupling proteins-2 expression.
XX PS Disclosure; Page 79; 80pp; English.
XX CC The invention relates to a method of diagnosing occurrence of a stroke or
XX CC assessing a patient's susceptibility to a stroke, comprising detecting in
XX CC a patient sample an elevated level of uncoupling proteins (UCP)-2
XX CC expression. The method is useful for diagnosing occurrence of a stroke or
XX CC assessing a patient's susceptibility to a stroke, where the stroke is an
XX CC ischaemic stroke. The method is useful for treating a subject having or
XX CC is susceptible to a neurological disorder or a neuronal injury, where the
XX CC neuronal injury is a stroke, or an ischaemic stroke. The neurological
XX CC disorder is selected from Parkinson's disease, Huntington's disease,
XX CC inherited ataxia, motor neuron diseases, Alzheimer's disease, epilepsy,
XX CC and traumatic brain injury. The disorder is treated with a prophylactic
XX CC agent which increases the permeability of the blood/brain barrier, or
XX CC with an anticoagulant and a secondary agent selected from bradykinin,
XX CC serotonin, histamine and arachidonic acid. The agent is a purified
XX CC UCP-2 polypeptide in combination with an anticoagulant. The method is
XX CC also useful for screening for an agent useful for treating a neurological
XX CC disorder or a neuronal injury. The present sequence represents the
XX CC coding sequence of human UCP-2, the gene of which is located on
XX CC Chromosome 11.
XX SQ Sequence 930 BP; 185 A; 285 C; 255 G; 205 T; 0 other;
XX
XX Query Match 99.8%; Score 928.4; DB 24; Length 930;
XX Best Local Similarity 99.9%; Pred. No. 9.7e-239;
XX Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGTTGGCTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
DB 1 ATGGTTGGCTTCAAGGCCACAGATGTGCCCTTACTGCACTGTGAAGTTTCTTGAGGCT 60
QY 61 GGCACAGCTGCTGCACTGCAATCTCAATCACTTCTTCTGGAATACGTCTAAAGTCCGG 120
DB 61 GGCACAGCTGCTGCACTGCAATCTCAATCACTTCTTCTGGAATACGTCTAAAGTCCGG 120
QY 121 TTACAGATCCCAAGGAGAAAGTCAAGGGCCAGTGCAGGCTTACAGCCAGCCAGTACCGC 180
DB 121 TTACAGATCCCAAGGAGAAAGTCAAGGGCCAGTGCAGGCTTACAGCCAGCCAGTACCGC 180

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Db 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCGACGTAACCG 180
 QY 181 GGTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 GGTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 GGGCTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Db 241 GGGCTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 GATTCGTCAACAGATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 GATTCGTCAACAGATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 CTAGCAGGACGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 CTAGCAGGACGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 AAGTCCGATTCACAGCTCAGGCGGCTGAGAGTGTGAGATGACCAAGGACCGTC 480
 Db 421 AAGTCCGATTCACAGCTCAGGCGGCTGAGAGTGTGAGATGACCAAGGACCGTC 480
 QY 481 AATGCTACAGACCATTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 Db 481 AATGCTACAGACCATTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 CCCAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 541 CCCAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 601 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Db 601 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 661 GCGTTGGGGGAGGCTTCTGACACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 661 GCGTTGGGGGAGGCTTCTGACACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 QY 721 AGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 Db 721 AGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 CTCCAG 840
 Db 781 CTCCAG 840
 QY 841 GGTTCCTGAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 Db 841 GGTTCCTGAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 GCGTGCATCTCCGAGAGGCTCCCTTCTGA 930
 Db 901 GCGTGCATCTCCGAGAGGCTCCCTTCTGA 930
 RESULT 11
 ID AAV82381 standard; DNA; 1596 BP.
 XX AAV82381;
 DE 31-MAR-1999 (first entry)
 XX Full length human C5 nucleotide sequence.
 KW Body weight disorder; obesity; appetite regulation; thermoregulation;
 KW anorexia; abnormal food intake; cachexia; thermogenesis; ss.
 OS Homo sapiens.
 PN US5853975-A.
 XX 29-DEC-1998.
 PD

XX 26-FEB-1997; 97US-0807861.
 PF 26-FEB-1997; 97US-0807861.
 PR 26-FEB-1997; 97US-0807861.
 PR 23-AUG-1994; 94US-0284522.
 PR 06-JUN-1995; 95US-0470868.
 PR 23-AUG-1995; 95US-0518878.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Targatella LA;
 DR WPI: 1999-094892/08.
 DR P-PDBE: AAM89546.
 PT Identifying modulators of C5 protein uncoupling activity - used as
 PT potential regulators of thermogenesis, appetite and body weight,
 PT e.g. for treating obesity, anorexia and cachexia
 PS Example: Fig 18; 83bp; English.
 CC The present invention describes a method for identifying a compound (I)
 CC that modulates C5 protein uncoupling activity by: (a) treating a test
 CC compound with C5 or cells expressing it; (b) measuring the level of
 CC uncoupling activity; and (c) comparing this with level of activity in
 CC the absence of the test compound. Any difference in the levels indicates
 CC a modulator. C5 protein has uncoupling activity, i.e. it can transport
 CC protons across the mitochondrial inner membrane, reducing the proton
 CC motive force and allowing dissipation of caloric energy as heat. It is
 CC thus a regulator of thermogenesis and is involved in body weight
 CC regulation. (I) are potentially useful in treatment of body weight
 CC disorders, regulation of appetite and thermoregulation, e.g. in cases of
 CC obesity, anorexia, abnormal food intake and cachexia. The present
 CC sequence represents the full length human C5 nucleotide sequence, from
 CC the present invention.
 SQ Sequence 1596 BP; 319 A; 506 C; 384 G; 387 T; 0 other;
 Query Match 99.8%; Score 928.4; DB 20; Length 1596;
 Best Local Similarity 99.9%; Pred. No. 1.2e-238;
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGGTGGGTTCAAGGCGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
 Db 313 ATGGTGGGTTCAAGGCGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 372
 QY 61 GGCACAGTGCCTCATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Db 373 GGCACAGTGCCTCATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
 QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTTACAGCCGCCAGTACCGG 180
 Db 433 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTTACAGCCGCCAGTACCGG 492
 QY 433 GGTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 GGTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 GGGCTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 Db 553 GGGCTGATGGGACCATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 301 GATTCGTCAACAGATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 613 GATTCGTCAACAGATCTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 CTAGCAGGACGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 673 CTAGCAGGACGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 421 AAGTCCGATTCACAGCTCAGGCGGCTGAGAGTGTGAGATGACCAAGGACCGTC 480
 Db 733 AAGTCCGATTCACAGCTCAGGCGGCTGAGAGTGTGAGATGACCAAGGACCGTC 792

QY	481	AATGCTCTCAGAACCATATGCCCCGAGAGGAAGGGCTCCGAGGCTCTGAAAGGGACCTCT	540
Db	793	AATGCTCTCAGAACCATATGCCCCGAGAGGAAGGGCTCCGAGGCTCTGAAAGGGACCTCT	852
QY	541	CCCAATGTTGCTCGTAATGCACTGTGTCACTGTGTGAGCTGTGTGACCTATATGACTATATC	600
Db	853	CCCAATGTTGCTCGTAATGCACTGTGTCACTGTGTGAGCTGTGTGACCTATATGACTATATC	912
QY	601	AAGGATGCGCTCCTTAAGAGCCAACTCATGACAGATGACCTCCCTTGACCATTCACTCTCT	660
Db	913	AAGGATGCGCTCCTTAAGAGCCAACTCATGACAGATGACCTCCCTTGACCATTCACTCTCT	972
QY	661	GCGTTTGGGGAGGGCTTTTGCAACCACTGTCAATGCGCTCCCTGTAGACGTGTCTAAGACG	720
Db	973	GCGTTTGGGGAGGGCTTTTGCAACCACTGTCAATGCGCTCCCTGTAGACGTGTCTAAGACG	1032
QY	721	AGATATATGAATCTGTGCGCCCTGGGCGCAAGTAAAGTAAAGGCTGGGCACTGTGACCTTTACAG	780
Db	1033	AGATATATGAATCTGTGCGCCCTGGGCGCAAGTAAAGTAAAGGCTGGGCACTGTGACCTTTACAG	1092
QY	781	CTTCAGAAAGAGGGGCCCCGAGCGCTTTACAAAGGTTCAATGCCCTCTTTCTCCGCTTG	840
Db	1093	CTTCAGAAAGAGGGGCCCCGAGCGCTTTACAAAGGTTCAATGCCCTCTTTCTCCGCTTG	1152
QY	841	GGTTCCTGGAACGTGTGATGTTGTCACCTATATGAGTAGCTGAAAGAGGCTCTATGAGCT	900
Db	1153	GGTTCCTGGAACGTGTGATGTTGTCACCTATATGAGTAGAGCTGAAAGAGGCTCTATGAGCT	1212
QY	901	GCGTCACCTTCCGAGAGGCTCCCTTTGCA	930
Db	1213	GCGTCACCTTCCGAGAGGCTCCCTTTGCA	1242

Db 1153 GGTTCCTGGAACTGGTGATGTTGTCACCTTANGAGACGTAAGACGCTCATG3CT 1212

QY 901 GCTTGCACTCCCGAGAGGCTCCTTCTGA 930

Db 1213 GCTTGCACTCCCGAGAGGCTCCTTCTGA 1242

RESULT 13

AAA52254

ID AAA52254 standard; cDNA; 1596 BP.

AC AAA52254;

XX 18-SEP-2000 (first entry)

DE Human uncoupling protein C5 cDNA, SEQ ID NO:38.

XX Body weight disorder; obesity; cachexia; differential expression;

KM human; C5 gene; C5 protein; UCP homologue; uncoupling protein;

KW thermogenesis; expression modulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 313..1242

FT /tag= a

FT /product= "Human C5 uncoupling protein"

XX US6057109-A.

XX 02-MAY-2000.

XX 14-DEC-1998; 98US-0210681.

XX 26-FEB-1997; 97US-0807861.

PR 08-OCT-1997; 97US-0946713.

PR 23-AUG-1994; 94US-0294522.

PR 06-JUN-1995; 95US-0470868.

PR 23-AUG-1995; 95US-0518878.

XX (MILL-) MILLENNIUM PHARM INC.

XX Tartaglia LA;

PI WPI; 2000-338601/29.

DR P-PSDB; AA97998.

XX Identifying C5 gene expression modulators useful for treating obesity

PT and cachexia comprises comparing levels of C5 expression prior to or

PT after contacting it with test compound

XX Examples; Fig 18A-B; 84p; English.

XX The invention relates to a method for identifying a compound that

CC modulates expression of the novel gene C5. The method comprises

CC contacting a cell expressing the C5 protein with a test compound, and

CC comparing the levels of C5 expression prior to or after exposure to the

CC test compound. A difference in expression indicates that the test

CC compound is a C5 gene expression modulator. The C5 protein (AA97997,

CC AA97998) has sequence similarity with mammalian brown fat uncoupling

CC proteins (UCPs). In the exemplifications of the invention, the C5

CC protein was shown to be able to uncouple ATP synthesis from oxidative

CC phosphorylation, allowing caloric energy to be dissipated as heat. cDNA

CC sequences encoding C5 (AAA52253, AAA52254) were isolated in an

CC investigation to identify genes which are differentially expressed in

CC body weight disorders such as obesity and cachexia. A compound which

CC modulates C5 expression is useful for modulating thermogenesis, and is

CC therefore useful for treating body weight disorders. Increasing the level

CC of C5 gene expression and/or gene product activity increases the rate of

CC thermogenesis and causes a reduction in body weight, which is useful for

CC the treatment of obesity. Decreasing the level of C5 gene expression

CC and/or C5 gene product activity decreases the rate of thermogenesis

CC and causes an increase in body weight, which is useful for the treatment

CC of cachexia. The present sequence represents a full-length cDNA clone

CC encoding the human C5 protein.

XX SQ Sequence 1596 BP; 319 A; 506 C; 384 G; 387 T; 0 other;

Query Match 99.8%; Score 928.4; DB 21; Length 1596;

Best Local Similarity 99.9%; Pred. No. 1.2e-238;

Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGCACAGATGATGCCCCCTACTGCTCCAGCTGTGAAGTTCTTGGGGCT 60

Db 313 ATGGTTGGGTTCAAGGCGCACAGATGATGCCCCCTACTGCTCCAGCTGTGAAGTTCTTGGGGCT 372

QY 61 GGCACAGCTGCTGCATCCGAGATCTCATACCTTCCCTGGAATATCTGAAGCCG 120

Db 373 GGCACAGCTGCTGCATCCGAGATCTCATACCTTCCCTGGAATATCTGAAGCTCCG 432

QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCGCAATACCGC 180

Db 433 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCCGCAATACCGC 492

QY 181 GGTGTGATGGGACCATTCATGACCATGTGCGCTACAGAGGCGCCCGAAGCCTTCAAT 240

Db 493 GGTGTGATGGGACCATTCATGACCATGTGCGCTACAGAGGCGCCCGAAGCCTTCAAT 552

QY 241 GGGCTGTTGCGGCGCTGCAGCGCCAAATGAGCTTTGCCCTGTCCGATCGGCGCTGAT 300

Db 553 GGGCTGTTGCGGCGCTGCAGCGCCAAATGAGCTTTGCCCTGTCCGATCGGCGCTGAT 612

QY 301 GATTCTGTCAAAAGTTCTACACCAAGGGCTTGACCAATGCGACATGCGAGTGGAGCGCGCTC 360

Db 613 GATTCTGTCAAAAGTTCTACACCAAGGGCTTGACCAATGCGACATGCGAGTGGAGCGCGCTC 672

QY 361 CTAGCAGGACAGCACACAGGTGCGCTGTGCTGTGCTGTGAGCCGACCGACGATGTGTA 420

Db 673 CTAGCAGGACAGCACACAGGTGCGCTGTGCTGTGCTGTGAGCCGACCGACGATGTGTA 732

QY 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGTGAGGTGTGTGGAGATACCAAAAGCAACCGTC 480

Db 733 AAGTCCGATTCCAGCTCAGGCGCGGCTGTGAGGTGTGTGGAGATACCAAAAGCAACCGTC 792

QY 481 AATGCTCAAGAACCATTTGCGCGAGAGAAAGGTTCCGGGCGCTCTGAAAGGACCTCT 540

Db 793 AATGCTCAAGAACCATTTGCGCGAGAGAAAGGTTCCGGGCGCTCTGAAAGGACCTCT 852

QY 541 CCAATGTGCTCGTAATGCCATTGTCACTGTGCTGAGTGTGACCTTATGACCTTATC 600

Db 853 CCAATGTGCTCGTAATGCCATTGTCACTGTGCTGAGTGTGACCTTATGACCTTATC 912

QY 601 AAGATGCGCTCTGAAAGCCAACTCATGACAGATGACTCCCTTGCCACTTCACTTCT 660

Db 913 AAGATGCGCTCTGAAAGCCAACTCATGACAGATGACTCCCTTGCCACTTCACTTCT 972

QY 661 GCTTTGGGGGAGGCTTTGTGACCACTGTATGCTCCCTCTGAAAGCTGTGTAAGAGC 720

Db 973 GCTTTGGGGGAGGCTTTGTGACCACTGTATGCTCCCTCTGAAAGCTGTGTAAGAGC 1032

QY 721 AGATCATGAATCTGCGCCCTGGGCACTAGTAGAGCTGCGCACTGTGCGCTTACATG 780

Db 1033 AGATCATGAATCTGCGCCCTGGGCACTAGTAGAGCTGCGCACTGTGCGCTTACATG 1092

QY 781 CTCGAAAGAGAGGGGCGCCGAGCTTCTTCAAAAGGTTCAATGCTCTCTTCTTCCGCTTG 840

Db 1093 CTCGAAAGAGAGGGGCGCCGAGCTTCTTCAAAAGGTTCAATGCTCTCTTCTTCCGCTTG 1152

QY 841 GGTTCCTGGAAGCTGTGATGTTGTGACCTTATGAGAGCTGAAGAGCCTCATAGGCT 900

Db 1153 GGTTCCTGGAAGCTGTGATGTTGTGACCTTATGAGAGCTGAAGAGCCTCATAGGCT 1212

QY 901 GCTTGCACTCCCGAGAGGCTCCTTCTGA 930

Db 1213 GCTTGCACTCCCGAGAGGCTCCTTCTGA 1242

Db	1155	GGTTCCTGGAACGTGATGTTGTCACCTATGAGAGAGCTGAAACGAGCCCTCATGGCT	1214
Qy	901	GCCTGCACTTCCCGAGAGAGGCTCCCTTCTGA	930
Db	1215	GCCTGCACTTCCCGAGAGGCTCCCTTCTGA	1244

Search completed: February 4, 2004, 18:26:04
Job time : 315 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 18:07:02 : Search time 75 Seconds

(without alignments)
5473.151 Million cell updates/sec

Title: US-09-884-814-2

Perfect score: 930
Sequence: 1 atcggttg99gttcaggccac.....cccgagagctccctctcga 930

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Parents NA: *
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6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	928.4	99.8	1536	2 US-08-807-861A-38	Sequence 38, Appl
2	928.4	99.8	1536	3 US-09-210-681-38	Sequence 38, Appl
3	928.4	99.8	1536	3 US-08-946-719A-38	Sequence 38, Appl
4	928.4	99.8	1536	4 US-09-547-983-38	Sequence 38, Appl
5	888.4	96.6	1255	1 US-08-518-878B-38	Sequence 38, Appl
6	888.4	96.6	1255	1 US-08-294-522B-38	Sequence 38, Appl
7	888.4	96.6	1255	2 US-08-470-868A-38	Sequence 38, Appl
8	888.4	96.6	1255	2 US-08-518-878B-38	Sequence 38, Appl
9	618	66.5	1205	1 US-08-518-878B-37	Sequence 36, Appl
10	618	66.5	1205	1 US-08-294-522B-37	Sequence 36, Appl
11	618	66.5	1205	2 US-08-807-861A-36	Sequence 36, Appl
12	618	66.5	1205	3 US-09-210-681-36	Sequence 36, Appl
13	618	66.5	1205	3 US-08-946-719A-36	Sequence 36, Appl
14	618	66.5	1205	4 US-09-547-983-36	Sequence 36, Appl
15	508.8	54.7	512	4 US-09-702-705-1014	Sequence 1014, Ap
16	508.8	54.7	512	4 US-09-736-457-1014	Sequence 1014, Ap
17	472.4	50.8	1192	3 US-09-142-565-1	Sequence 1, Appl
18	472.4	50.8	1192	3 US-08-937-466-1	Sequence 1, Appl
19	471.8	50.7	2782	2 US-09-172-528-1	Sequence 1, Appl
20	471.8	50.7	2782	3 US-09-318-199-1	Sequence 1, Appl
21	471.8	50.7	2782	3 US-09-503-579-1	Sequence 1, Appl
22	469.2	50.5	1949	2 US-08-937-466-3	Sequence 3, Appl
23	469.2	50.5	1949	2 US-09-172-528-3	Sequence 3, Appl
24	469.2	50.5	1949	3 US-09-318-199-3	Sequence 3, Appl
25	469.2	50.5	1949	3 US-09-503-579-3	Sequence 3, Appl
26	390.6	42.0	1777	2 US-08-937-466-5	Sequence 5, Appl
27	390.6	42.0	1777	2 US-08-172-528-5	Sequence 5, Appl

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29	390.6	42.0	1777	3 US-09-503-579-5	Sequence 5, Appl
30	316.4	34.0	318	4 US-09-702-705-1376	Sequence 1376, Ap
31	316.4	34.0	318	4 US-09-736-457-1376	Sequence 1376, Ap
32	241.8	26.0	309	1 US-08-518-878B-14	Sequence 14, Appl
33	241.8	26.0	309	1 US-08-294-522B-14	Sequence 14, Appl
34	241.8	26.0	309	2 US-08-807-861A-14	Sequence 14, Appl
35	241.8	26.0	309	2 US-08-470-868A-14	Sequence 14, Appl
36	241.8	26.0	309	3 US-09-210-681-14	Sequence 14, Appl
37	241.8	26.0	309	3 US-08-946-719A-14	Sequence 14, Appl
38	241.8	26.0	309	4 US-09-547-983-14	Sequence 14, Appl
39	178.6	19.2	847	3 US-09-142-565-5	Sequence 5, Appl
40	111.6	12.0	309	1 US-08-518-878B-15	Sequence 15, Appl
41	111.6	12.0	309	1 US-08-294-522B-15	Sequence 15, Appl
42	111.6	12.0	309	2 US-08-807-861A-15	Sequence 15, Appl
43	111.6	12.0	309	2 US-08-470-868A-15	Sequence 15, Appl
44	111.6	12.0	309	3 US-09-210-681-15	Sequence 15, Appl
45	111.6	12.0	309	3 US-08-946-719A-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-807-861A-38
Sequence 38, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Targadia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITL OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518, 878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470, 868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294, 522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION/DOCKET NUMBER: 30, 742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-807-861A-38
Query Match 99.8%; Score 928.4; DB 2; Length 1536;

Best Local Similarity 99.9%; Pred. No. 7.9e-242;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATGGTGGGTTCAAGGCCACAGATGTGGCCCTTACCTGCACTGTGAAGTTTCTTGGGGCT 60
DB 313 ATGGTGGGTTCAAGGCCACAGATGTGGCCCTTACCTGCACTGTGAAGTTTCTTGGGGCT 372
QY 61 GGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 373 GGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
QY 121 TTACAGATCCAAAGAGAAAGTCAAGGAGGAGTCAAGGAGGAGTCAAGGAGGAGTCAAG 180
DB 433 TTACAGATCCAAAGAGAAAGTCAAGGAGGAGTCAAGGAGGAGTCAAGGAGGAGTCAAG 492
QY 181 GGTGTGATGGGAGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 493 GGTGTGATGGGAGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 241 GGGCTGTGGCCGCTGCAAGCCCAATGAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGT 300
DB 553 GGGCTGTGGCCGCTGCAAGCCCAATGAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGT 612
QY 301 GATTGTGCAAAAGTTTCTACACCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 360
DB 613 GATTGTGCAAAAGTTTCTACACCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 672
QY 361 CTAGCAGGAGCAGCAGCAGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 420
DB 673 CTAGCAGGAGCAGCAGCAGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 732
QY 421 AAGGTCCGATTCAGAGCTCAGGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 480
DB 733 AAGGTCCGATTCAGAGCTCAGGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 792
QY 481 AATGCTTCAAGAGCATTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 793 AATGCTTCAAGAGCATTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 852
QY 541 CCCAATGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 853 CCCAATGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 912
QY 601 AAGATGCGCTCTCTGAAAGCCAACTCATGACAGATGATGATGATGATGATGATGATGAT 660
DB 913 AAGATGCGCTCTCTGAAAGCCAACTCATGACAGATGATGATGATGATGATGATGATGAT 972
QY 661 GCGTTTGGGAGGAGGCTTGTGACCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 973 GCGTTTGGGAGGAGGCTTGTGACCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1032
QY 721 AAGTACATGAACTGCGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 1033 AAGTACATGAACTGCGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1092
QY 781 CTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 1093 CTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1152
QY 841 GGTTCCTGGAAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 1153 GGTTCCTGGAAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1212
QY 901 GGCTGCACTTCCGAGAGAGGCTTCCCTTCTGA 930
DB 1213 GGCTGCACTTCCGAGAGAGGCTTCCCTTCTGA 1242

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RESULT 2
US-09-210-681-38
Sequence 38, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:

```

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-210-681-38
Query Match 99.8%; Score 926.4; DB 3; Length 1596;
Best Local Similarity 99.9%; Pred. No. 7.9e-242;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGTGGGTTCAAGGCCACAGATGTGGCCCTTACCTGCACTGTGAAGTTTCTTGGGGCT 60
DB 313 ATGGTGGGTTCAAGGCCACAGATGTGGCCCTTACCTGCACTGTGAAGTTTCTTGGGGCT 372
QY 61 GGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 373 GGCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 432
QY 121 TTACAGATCCAAAGAGAAAGTCAAGGAGGAGTCAAGGAGGAGTCAAGGAGGAGTCAAG 180
DB 433 TTACAGATCCAAAGAGAAAGTCAAGGAGGAGTCAAGGAGGAGTCAAGGAGGAGTCAAG 492
QY 181 GGTGTGATGGGAGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 493 GGTGTGATGGGAGCAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 552
QY 241 GGGCTGTGGCCGCTGCAAGCCCAATGAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 300
DB 553 GGGCTGTGGCCGCTGCAAGCCCAATGAGCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 612
QY 301 GATTGTGCAAAAGTTTCTACACCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 360
DB 613 GATTGTGCAAAAGTTTCTACACCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 672

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QY	36	CTAGAGAGGACAGACCAAGGAGCCCTGGCTGTGGCTGTGGCTGGCCAGCCACGGATGTG37A	420
Db	673	CTAGAGGACGACACCAAGGAGCCCTGGCTGTGGCTGTGGCTGGCCAGCCACGGATGTG67A	732
QY	421	AAGGTCGATTCCTCAAGCTCAGGCCCCGCGCTGAGGTGTGTGGATATCAAGACCGCTC	480
QY	481	AATGCGCTCAAGACCATTCGAGCCCGAGAGAAAGGATCCGAGGCGCTCTGGAGAAAGGACCTCT	540
Db	793	AATGCGCTCAAGACCATTCGAGCCCGAGAGAAAGGATTCGAGGCGCTCTGGAGAAAGGACCTCT	852
QY	541	CCCAATGTTGCTGTATATGCAATTCGATCTGTGCTGAGCTGTGATCTATGACCTCTATC	600
QY	853	CCCAATGTTGCTGTATATGCAATTCGATCTGTGCTGAGCTGTGATCTATGACCTCTATC	912
Db	601	AAGGATGCCCCCTCTTAAGAGCCCAACCTCATGACAGATGACCTCCCTTGACCATTCATCTCT	660
Db	913	AAGGATGCCCCCTCTTAAGAGCCCAACCTCATGACAGATGACCTCCCTTGACCATTCATCTCT	972
QY	661	GCCTTGTGGGAGGAGCTTCTGACCACTGTATCGCCTCCCTGTAGACGTGTGACAGG	720
Db	973	GCCTTGTGGGAGGAGCTTCTGACCACTGTATCGCCTCCCTGTAGACGTGTGACAGG	1032
QY	721	AAGTATATTAATCTGCTGCTGCTGAGGAGATGACATGAGCGCTGGAGCATGTGACCTTACATG	780
Db	1033	AAGTATATTAATCTGCTGCTGCTGAGGAGATGACATGAGCGCTGGAGCATGTGACCTTACATG	1092
QY	781	CTCCAGAGAGAGAGGAGGAGCCCGAGAGCTTCTCAAAAGGATTCATGCCCCCTTCTCCGCTTG	840
Db	1093	CTCCAGAGAGAGAGGAGGAGCCCGAGAGCTTCTCAAAAGGATTCATGCCCCCTTCTCCGCTTG	1152
QY	841	GGTCTCTGGAACGTGTATATGTTGTCACTATGAGAGCATGAGATGAAAGAGCCCTCATGTGCT	900
Db	1153	GGTCTCTGGAACGTGTATATGTTGTCACTATGAGAGCATGAGATGAAAGAGCCCTCATGTGCT	1212
QY	901	GCCTGCACTCCCGAGAGGAGCTCCCTTCTGA	930
Db	1213	GCCTGCACTCCCGAGAGGAGCTCCCTTCTGA	1242
RESULT 3			
US-08-946-719A-38			
Sequence 38, Application US/08946719A			
Patent No. 6121017			
GENERAL INFORMATION:			
APPLICANT: Tartaglis, Louis A.			
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND			
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY			
NUMBER OF SEQUENCES: 64			
CORRESPONDENCE ADDRESSES:			
ADDRESSEE: Pennie & Edmonds LLP			
STREET: 1155 Avenue of the Americas			
CITY: New York			
STATE: New York			
COUNTRY: U.S.A.			
ZIP: 10036-2711			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/946,719A			
FILING DATE: 8-OCT-1997			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 08/807,861			
FILING DATE: 26-FEB-1997			
APPLICATION NUMBER: US 08/518,878			
FILING DATE: 23-AUG-1995			
APPLICATION NUMBER: US 08/470,868			

	Filing Date:	06-JUN-1995
	Application Number:	US 08/294,522
	Filing Date:	23-AUG-1994
	Attorney/Agent Information:	
	Name:	Cortuzzi, Laura A.
	Registration Number:	30,742
	Reference/Docket Number:	7853-107
	Telecommunication Information:	
	Telephone:	(212) 790-9090
	Telefax:	(212) 869-9741/8864
	Telex:	66141 PENNIE
	Information for SEQ ID NO:	38:
	Sequence Characteristics:	
	Length:	1596 base pairs
	Type:	nucleic acid
	Strandedness:	single
	Topology:	linear
	Molecule Type:	DNA
	US-08-946-719A-38	
Query Match	99.8%; Score 928.4; DB 3;	Length 1596;
Best Local Similarity	99.9%; Pred. No. 7.9e-242;	
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1 ATGCTTGGGTTCMAECCCAAGATGTCGCCCTTAACCTGAAGACTTTCTTGAGGCT	60
DB	313 ATGGTTGGGTTCMAEGGCACAGATGTCCCCCTACCTGCACCTGTGAATTCTTGGAGCT	372
QY	61 GCACAGCGCTGCGCATGAGATCTGATCACCCTTCTCTGGATACTGCTAAAGTCGGG	120
DB	373 GGACAGCGCTGCGCATGTGAGATCTCATCACCTTCTCTGGATACTGCTAAAGTCGGG	432
QY	121 TTACAGATCCAAAGGAAGAAGTCAAGGGGCGCTGCGCGCTACACGACGCGCCACATACGC	180
DB	433 TTACAGATCCAAAGGAAGAAGTCAAGGGGCGCTGCGCGCTACACGACGCGCCACATACGC	492
QY	181 GGATGATATGGGACCATCTTACCATGTGCTGCTACTGAGGGCCCGGAAAGCTCTACAT	240
DB	493 GGATGATATGGGACCATCTTACCATGTGCTGCTACTGAGGGCCCGGAAAGCTCTACAT	552
QY	241 GGGCTGGTTCGGGCTTGACGCGCCAAATGAGCTTTGCTCTGTCCGATCGGCTGAT	300
DB	553 GGGCTGGTTCGGGCTTGACGCGCCAAATGAGCTTTGCTCTGTCCGATCGGCTGAT	612
QY	301 GATTCGTCAAACAATTCATCAACAAGGGCTCTGAGATGCGACGATTTGGAGCGCGCTC	360
DB	613 GATTCGTCAAACAATTCATCAACAAGGGCTCTGAGATGCGACGATTTGGAGCGCGCTC	672
QY	361 CTAGCAGGACGACCAAGATGCGCTGTGCTGTGCTGTGGCCGACCGACCGATGTGTA	420
DB	673 CTAGCAGGACGACCAAGATGCGCTGTGCTGTGCTGTGGCCGACCGACCGATGTGTA	732
QY	421 AAGTCCGATTTCCAAGCTCAGGCCCAGGCTCTGAGAGTGTCTGGAGATACCAAGACACCGTC	480
DB	733 AAGTCCGATTTCCAAGCTCAGGCCCAGGCTCTGAGAGTGTCTGGAGATACCAAGACACCGTC	792
QY	481 AATGCTTACAAAGCATTTGCGGAGAGAGGTTCCGGGGCTCTGTGAAAAGGACCTCT	540
DB	793 AATGCTTACAAAGCATTTGCGGAGAGAGGTTCCGGGGCTCTGTGAAAAGGACCTCT	852
QY	541 CCCAATGTTGCTGTGAATGCAATGTCTCACTGTGCTGAGCTGGTGAACCTATGACCTCATC	600
DB	853 CCCAATGTTGCTGTGAATGCAATGTCTCACTGTGCTGAGCTGGTGAACCTATGACCTCATC	912
QY	601 AACGATGCGCTCTGAAAGCAACCTATGACAGATGACCTCCCTTGCACCTTCACTTCT	660
DB	913 AACGATGCGCTCTGAAAGCAACCTATGACAGATGACCTCCCTTGCACCTTCACTTCT	972
QY	661 GCGTTTGGGACAGGCTTCTGACCACTGTCAATGCGCTTCCCTGTGAACGTGGTCAAAGAC	720
DB	973 GCGTTTGGGACAGGCTTCTGACCACTGTCAATGCGCTTCCCTGTGAACGTGGTCAAAGAC	1032
QY	721 AGATACATGAATCTGCGCCTGGGACCAAGTACAGTAGCGCTGCGACCTGTGCGCTTACATG	780

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/518,878B
 FILING DATE: 23-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Cornuzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-036
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1255 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-518-878B-38

Query Match 96.6%; Score 898.4; DB 1; Length 1255;
 Best Local Similarity 99.9%; Pred. No. 9.5e-234;
 Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

31 CCTACGCACTGTAAGTTCTTGGGGCTGCGACAGCTGCTGCATGCGAGATCTATC 90
 1 CCTACTGCCACTGTGAAGTTCTTGGGGCTGCGACAGCTGCTGCATGCGAGATCTATC 60
 91 ACCTTCTCTGTGATTAAGTCCGGTTACAGATCCAAAGGAAAGTCAGAGGCCA 150
 61 ACCTTCTCTGTGATTAAGTCCGGTTACAGATCCAAAGGAAAGTCAGAGGCCA 120
 151 GTGCGGCTACAGAGCCGCAAGTACCGGGTGTGATGAGGCGACCATTTCTGACATG 210
 121 GTGCGGCTACAGAGCCGCAAGTACCGGGTGTGATGAGGCGACCATTTCTGACATG 180
 211 CGTACTGAGAGGCCCGGAGAGCTCTACATGAGGCTGTGCGCGGCTGCAAGCCCAATG 270
 181 CGTACTGAGAGGCCCGGAGAGCTCTACATGAGGCTGTGCGCGGCTGCAAGCCCAATG 240
 271 AGCTTGTCTGTCTGCGCATGCGCTGTATGATTTCTGTCAACAGTTTCTACACCAAGGCC 330
 241 AGCTTGTCTGTCTGCGCATGCGCTGTATGATTTCTGTCAACAGTTTCTACACCAAGGCC 300
 331 TCTGAGCATGCGAGCATTTGGAGAGCGCTCTTACAGAGCAGACACAGAGTCCCTGCT 390
 301 TCTGAGCATGCGAGCATTTGGAGAGCGCTCTTACAGAGCAGACACAGAGTCCCTGCT 360
 391 GTGCGTGTGCGCCCAAGCCAGATGTGTAAAGTCCGATTTCAAGCTCAGCGCGGCT 450
 361 GTGCGTGTGCGCCCAAGCCAGATGTGTAAAGTCCGATTTCAAGCTCAGCGCGGCT 420
 451 GGAAGTGTGCGAGATACCAAGCAAGCCCAATGTCTTCAAGACCATTTGCCGAGAGAA 510
 421 GGAAGTGTGCGAGATACCAAGCAAGCCCAATGTCTTCAAGACCATTTGCCGAGAGAA 480
 511 GGGTTCCGGGGCTCTTGAAAGGAGCTTCCCAATGTTGCTGTATGCAATTTGTCAAC 570
 481 GGGTTCCGGGGCTCTTGAAAGGAGCTTCCCAATGTTGCTGTATGCAATTTGTCAAC 540
 571 TGTGCTGAGTGTGACATATACCTCATCAAGAGATGCCCTCTGAAAGCAACTCATG 630

541 TGTGCTGAGTGTGACATATACCTCATCAAGAGATGCCCTCTGAAAGCAACTCATG 600
 631 ACAGATGACCTCTCTTGGCACTTACTTCTGCTTTGGGAGAGCTTTGCAACCAATGTC 690
 601 ACAGATGACCTCTCTTGGCACTTACTTCTGCTTTGGGAGAGCTTTGCAACCAATGTC 660
 691 ATCCGCTCCCTGTAGACGTGTGCAAGACGATATACATCTCCCTGAGGCGAGTAC 750
 661 ATCCGCTCCCTGTAGACGTGTGCAAGACGATATACATCTCCCTGAGGCGAGTAC 720
 751 AGTACGCTGCGCACTGTGCTTACATGCTTCAAGAGAGGGGCGCCGAGGCTTCTAC 810
 721 AGTACGCTGCGCACTGTGCTTACATGCTTCAAGAGAGGGGCGCCGAGGCTTCTAC 780
 811 AAAGGTTTCAAGCCCTCTTCTTCCGCTGTGGTTCCTGGAACGTGTGATGTTGTCACC 870
 781 AAAGGTTTCAAGCCCTCTTCTTCCGCTGTGGTTCCTGGAACGTGTGATGTTGTCACC 840
 871 TATGACAGCTGAAACGAGCCCTCATGAGTGTGCTGCACTTCCGAGAGGCTCCCTTCTGA 930
 841 TATGACAGCTGAAACGAGCCCTCATGAGTGTGCTGCACTTCCGAGAGGCTCCCTTCTGA 900

RESULT 6

US-08-294-522B-38

Sequence 38, Application US/08294522B

Patent No. 5741666

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: Compositions and Methods for the

TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,522B

FILING DATE: 23-AUG-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Cornuzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-015

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8664/9741

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 1255 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-294-522B-38

Query Match 96.6%; Score 898.4; DB 1; Length 1255;
 Best Local Similarity 99.9%; Pred. No. 9.5e-234;
 Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

31 CCTACGCACTGTAAGTTCTTGGGGCTGCGACAGCTGCTGCATGCGAGATCTATC 90
 1 CCTACTGCCACTGTGAAGTTCTTGGGGCTGCGACAGCTGCTGCATGCGAGATCTATC 60
 91 ACCTTCTCTGTGATTAAGTCCGGTTACAGATCCAAAGGAAAGTCAGAGGCCA 150

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Db      61  ACCCTTCCTGTGATCTGCTAAAGTCCGGTTACAGATCCAGAGAAAGTCAAGGAGCA 120
Qy      151  GTGCGGCTACAGCCAGCCAGCCAGTACCGCGGTGATGAGGACACATTTCTGACATGAGT 210
Db      121  GTGCGGCTACAGCCAGCCAGCCAGTACCGCGGTGATGAGGACACATTTCTGACATGAGT 180
Qy      211  CGTACTAGAGGCCCCCGAAGCTCTACATAGGCTGTTGCCGCTGACAGGCCCAATG 270
Db      181  CGTACTAGAGGCCCCCGAAGCTCTACATAGGCTGTTGCCGCTGACAGGCCCAATG 240
Qy      271  AGCTTGGCTCTGTCGGCATGAGCTGTATGATTTGTTGTTCAACAGTTCTACACAGGCG 330
Db      241  AGCTTGGCTCTGTCGGCATGAGCTGTATGATTTGTTGTTCAACAGTTCTACACAGGCG 300
Qy      331  TCTGAGCATGCGACATTTGAGAGCGGCTCTCTAGACAGGACACACAGGCTGCTGCT 390
Db      301  TCTGAGCATGCGACATTTGAGAGCGGCTCTCTAGACAGGACACACAGGCTGCTGCT 360
Qy      391  GTGCGTGTGCGCCAGCCCAAGGATGTGTAAAGTCCGATCCAGACTCAGGCGCGGCT 450
Db      361  GTGCGTGTGCGCCAGCCCAAGGATGTGTAAAGTCCGATCCAGACTCAGGCGCGGCT 420
Qy      451  GAGGTGTGCGGAGATACCAAGACCGGTCAATGCTTCAAGACCAATGCGCGAGAGAA 510
Db      421  GAGGTGTGCGGAGATACCAAGACCGGTCAATGCTTCAAGACCAATGCGCGAGAGAA 480
Qy      511  GGGTTCGGGGGCTCTTGAAAGGGAAGCTTCCCAATGTTGCTGTAATGCTGTCAC 570
Db      481  GGGTTCGGGGGCTCTTGAAAGGGAAGCTTCCCAATGTTGCTGTAATGCTGTCAC 540
Qy      571  TGTGTGAGCTGTGACCTATGACCTCATCAAGAGATGCTCTCTGAAAGCCCACTCATG 630
Db      541  TGTGTGAGCTGTGACCTATGACCTCATCAAGAGATGCTCTCTGAAAGCCCACTCATG 600
Qy      631  ACAATGACCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 690
Db      601  ACAATGACCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 660
Qy      691  ATCGCTCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 750
Db      661  ATCGCTCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 720
Qy      751  AGTAGCGCTGCGCACTGTGCTTACCATGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGG 810
Db      721  AGTAGCGCTGCGCACTGTGCTTACCATGCTTCAAGAGAGGAGGAGGAGGAGGAGGAGG 780
Qy      811  AAAGGTTTCATGCGCTCTCTTCTGCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGG 870
Db      781  AAAGGTTTCATGCGCTCTCTTCTGCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGG 840
Qy      871  TATGAGCAGCTGAAAGAGGCTTCAATGAGCTGCTGACCTTCCGAGAGGCTCTCTTCTGA 930
Db      841  TATGAGCAGCTGAAAGAGGCTTCAATGAGCTGCTGACCTTCCGAGAGGCTCTCTTCTGA 900

```

RESULT 7

US-08-470-868A-38
Sequence 38, Application US/08470868A

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-9999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8664
TELEX: 66441 PENNIE
INFORMATION FOR SEQ. ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-38

```

Query Match: 96.6%; Score 898.4; DB 2; Length 1255;
Best Local Similarity 99.9%; Pred. No. 5,5e-234;
Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      31  CCTACTGCCACTGTGAAGTTCTCTGGGGCTGGACAGCTGCTGCATGCAATCTCATC 90
Db      1  CTTACTGCCACTGTGAAGTTCTCTGGGGCTGGACAGCTGCTGCATGCAATCTCATC 60
Qy      91  ACCTTCTCTGTGATCTGCTAAAGTCCGTTTACAGATCCAGAGAAAGTCAAGGAGCA 150
Db      61  ACCTTCTCTGTGATCTGCTAAAGTCCGTTTACAGATCCAGAGAAAGTCAAGGAGCA 120
Qy      151  GTGGGCGCTACAGCCAGCGCCAGTACCGCGGTGATGAGGACCATTTCTGACATGAGT 210
Db      121  GTGGGCGCTACAGTACAGCCAGGCTGACCGCGGTGATGAGGACCATTTCTGACATGAGT 180
Qy      211  CGTACTAGAGGCCCCCGAAGCTCTTACAAATGAGGCTGAGTCCGCGCTGACAGGCCAATG 270
Db      181  CGTACTAGAGGCCCCCGAAGCTCTTACAAATGAGGCTGAGTCCGCGCTGACAGGCCAATG 240
Qy      271  AGCTTGGCTCTGTGCGCATGCGCTGTAATGTTCTGTAACAGTCTTCAACAGAGGC 330
Db      241  AGCTTGGCTCTGTGCGCATGCGCTGTAATGTTCTGTAACAGTCTTCAACAGAGGC 300
Qy      331  TCTGAGCATGCGACATTTGAGAGCGGCTCTTACAGGAGGACACACAGGCTGCTGCT 390
Db      301  TCTGAGCATGCGACATTTGAGAGCGGCTCTTACAGGAGGACACACAGGCTGCTGCT 360
Qy      391  GTGCGTGTGCGCCAGCCCAAGGATGTGTAAAGTCCGATCCAGACTCAGGCGCGGCT 450
Db      361  GTGCGTGTGCGCCAGCCCAAGGATGTGTAAAGTCCGATCCAGACTCAGGCGCGGCT 420
Qy      451  GAGGTGTGCGGAGATACCAAGACCGGTCAATGCTTCAAGACCAATGCGCGAGAGAA 510
Db      421  GAGGTGTGCGGAGATACCAAGACCGGTCAATGCTTCAAGACCAATGCGCGAGAGAA 480
Qy      511  GGGTTCGGGGGCTCTTGAAAGGGAAGCTTCCCAATGTTGCTGTAATGCTGTCAC 570
Db      481  GGGTTCGGGGGCTCTTGAAAGGGAAGCTTCCCAATGTTGCTGTAATGCTGTCAC 540
Qy      571  TGTGCTAGCTGTGACCTTATGACCTTCAATGAGATGCTCTGTAAGCCCACTCATG 630
Db      541  TGTGCTAGCTGTGACCTTATGACCTTCAATGAGATGCTCTGTAAGCCCACTCATG 600
Qy      631  ACAATGACCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 690
Db      601  ACAATGACCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 660
Qy      691  ATCGCTCTCTCTGACCTTCTGACCTTCTGAGGAGGAGCTTCTGACACATGTC 750

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APPLICATION NUMBER: US/08/294,522B
 FILING DATE: 23-AUG-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULAR TYPE: CDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..912
 US-08-294-522B-37

Query Match 66.5%; Score 618; DB 1; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6,8e-158;
 Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

1 ATGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGTCAGATGTTTCTTGGGGCT 60
 1 ATGTTGGTTCAGGCCACAGATGTGCCCCCTACTGTCAGATGTTTCTTGGGGCT 60
 61 GGACAGCTGCTGTCAGATGTCAGATCTATCACTTCTCTGATCTGCTAAAGTCCG 120
 61 GGACAGCTGCTGTCAGATGTCAGATCTATCACTTCTCTGATCTGCTAAAGTCCG 120
 121 TTACAGATCCAGAGGAAGTCAAGGGGCTGAGGCGCTGAGCCGACGCGCCGATACCG 180
 121 CTGACAGATCCAGAGGAAGTCAAGGGGCTGAGGCGCTGAGCCGACGCGCCGATACCG 180
 181 GGTGTGATGGGACCACTTCTGACATGTGTGCTACTGAGGGCCCCCGAAGCTTCAAT 240
 181 GGTGTGATGGGACCACTTCTGACATGTGTGCTACTGAGGGCCCCCGAAGCTTCAAT 240
 241 GGGCTGTGCTGCGGCTGAGAGCCCAATGAGCTTGGCTGTCCGATCGGCTGTAT 300
 241 GGGCTGTGCTGCGGCTGAGAGCCCAATGAGCTTGGCTGTCCGATCGGCTGTAT 300
 301 GACTGTGTCAACAGTCTACACCAAGGGCTCAAGGATGAGGATCGGAGCGGCTC 360
 301 GATTGTCAACAGTCTTACACCAAGGGCTCTGAGCATGTCAGCATTTGGAGCGGCTC 360
 361 CTAGCAGCAGACCAACAGGTGCTGTGTGTGTGCGCCAGCCGACGAGTGTGTA 420
 361 CTAGCAGCAGACCAACAGGTGCTGTGTGTGTGCGCCAGCCGACGAGTGTGTA 420
 421 AAGTCCGATTCAGAGCTCAGGCGGCTGAGGCTGTGAGGATTCAGAAAGCAGCTC 480
 421 AAGTCCGATTCAGAGCTCAGGCGGCTGAGGCTGTGAGGATTCAGAAAGCAGCTC 480
 481 AATGCTTACAGACCACTTCCCGAAGGAAGGTTCCGGGCTCTTGAAAGGAGCTCT 540
 481 AATGCTTACAGACCACTTCCCGAAGGAAGGTTCCGGGCTCTTGAAAGGAGCTCT 540
 541 CCCAATGTGCTGTATGCTCATTTGTCACTGTGTGTCAGCTGTGTAAGCTATGACTATC 600
 541 CCCAATGTGCTGTATGCTCATTTGTCACTGTGTGTCAGCTGTGTAAGCTATGACTATC 600
 601 AAGATGCTCTCTTGAAGCCCAACTGATGACATGATGATCTCTCTGCACTTCACTTCT 660
 601 AAGATGCTCTCTTGAAGCCCAACTGATGACATGATGATGATCTCTCTGCACTTCACTTCT 660
 661 GCCTTTGGGCGAGGCTTGTGACACTGTCTATGCTGCTCCCTGTGAGATGTGTCAAGAG 720

649 GCCTTGGGGGGGGCTTGTGACCAACCGTATGCTCCCTGTGATGTGTGTAAGAG 708
 721 AGATACATGATCTCTCTGAGCCAGTACAGTACGCTGTGCACTGTGCTTACATG 780
 709 AGATACATGATCTCTGAGCCAGTACAGTACGCTGTGCACTGTGCTTACATG 762
 781 CTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 763 TGCTCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 822
 841 GGTTCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
 823 GATTCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 882
 901 GCCTGACCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 930
 883 GCCTACCAATCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 912

RESULT 10
 US-08-807-861A-36
 Sequence 36, Application US/08807861A
 Patent No. 5853975
 GENERAL INFORMATION:
 APPLICANT: Tarragila, Louis A.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 TITRATION OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/807,861A
 FILING DATE: 26-FEB-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/518,878
 FILING DATE: 23-AUG-1995
 APPLICATION NUMBER: US 08/470,868
 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER: US 08/294,522
 FILING DATE: 23-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-066
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 INFO: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-807-861A-36

Query Match 66.5%; Score 618; DB 2; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6,8e-158;
 Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

1 ATGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGTCAGATGTTTCTTGGGGCT 60

Db 1 ATGGTTGGTTTAAAGCCACAGATGTGCCCCCAAGCACTGTAAGTTCTCTGGGGCT 60
 Qy 61 GGCACAGCTGCTGATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCGG 120
 Db 61 GGCACAGCTGCTGATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCGG 120
 Qy 121 TTACAGATCCAAAGAGAAAGTGAAGGGGCGAGTGGCGGTACAGCCAGCGCCAGTACCG 180
 Db 121 CTGCAGATCCAAAGGAGAGTGAAGGGGCTAGTGGCGCACCGAGCCAGCGCCAGTACCG 180
 Qy 181 GGTGTGATGGGACCACTTCTGACCAATGTGCGTACTGAGGCCCCCGAAGCTTTACAAT 240
 Db 181 GGGTTCTGGTACCACTTCTGACCAATGTGCGCTGAGGCGCACTGAGGCTTCAACAT 240
 Qy 241 GGGCTGGTGGCGGCGCTGAGCGCCAAATGAGCTTTGCTCTGTCGCGCTGAT 300
 Db 241 GGGCTGGTGGCGGCGCTGAGCGCCAGATGAGCTTTGCTCTGTCGCGCTGAT 300
 Qy 301 GATTCTGTCAAACAGTTTACACCAAGGGCTCTGAGCATGCGCAATTTGGAGCCGCTC 360
 Db 301 GACTCTGTCAAACAGTTTACACCAAGGGCTCAGAGCATGAGGCAATGGAGCGCGCTC 360
 Qy 361 CTGACAGGACAGCCACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 CTGACAGGACAGCCACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Qy 421 AAGTCCGATTCCAGCTGAGCGCGCGCTGAGAGTGTGAGAGATACCAAGACCGCTC 480
 Db 421 AAGTCCGCTTCCAGCTGAGCGCGCGCTGAGAGTGTGAGAGATACCAAGACCGCTC 480
 Qy 481 AATGCTTACAAAGCACTTCCCGGAGAGAGAGGTTCCGGGCTCTTGAAAGGAGCTCT 540
 Db 478 TCGAGCTTACAAAGCACTTCCCGGAGAGAGGTTCCGGGCTCTTGAAAGGAGCTCT 532
 Qy 541 CCCAATGTGCTGATATGCAATTTGCACTGTCTGAGCTGATGACTATGACTATC 600
 Db 533 -CCCAATGTGCTGATATGCAATTTGCACTGTCTGAGCTGATGACTATGACTATC 591
 Qy 601 AAGGATGCTCTCTGAAAGCCAACTCATGACATGACCTCTCTGCACTTCACTTCT 660
 Db 592 AAGGATGCTCTCTGAAAGCCAACTCATGACATGACCTCTCTGCACTTCACTTCT 648
 Qy 661 GCGTTGGGAGGAGCTTTCGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 649 GCGTTGGGAGGAGCTTTCGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
 Qy 721 AGATACATGAATCTGCTGAGCGCAATGACATGAGTGGCGCTGCTGCTGCTGCTGCTGCT 780
 Db 709 AGATACATGA--CTGCTGAGGCGCAATGACATGAGTGGCGCTGCTGCTGCTGCTGCTGCT 762
 Qy 781 CTCCAGAGAGAGGAGGCGCGCGCTTCTCAAGGGTTCATGCGCTCTCTCTGCGCTGCT 840
 Db 763 TGTCTGGAGAGAGGAGGCGCGCGCTTCTCAAGGGTTCATGCGCTCTCTCTGCGCTGCT 822
 Qy 841 GGTTCCTGAAACCTGTGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 823 GATCTCTGAAACCTGTGATGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
 Qy 901 GCTGCACTTCCGAGAGGCTCCCTTCTGA 930
 Db 883 GCTTACCAATCTGAGAGGCACTTCTGA 912

RESULT 11
 US-08-470-868A-36
 ; Sequence 36, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tactagila, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TREATMENT OF Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie and Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,868A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-0031-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66441 PENNIE
 INFORMATION FOR SEO ID NO.: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-470-868A-36

Query Match 66.5%; Score 618; DB 2; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6,8e-158; Indels 18; Gaps 6;
 Matches 777; Conservative 0; Mismatches 135;

Qy 1 ATGGTTGGTTTCAAGCCACAGATGTGCCCCCAAGCACTGTAAGTTCTCTGGGGCT 60
 Db 1 ATGGTTGGTTTCAAGCCACAGATGTGCCCCCAAGCACTGTAAGTTCTCTGGGGCT 60
 Qy 61 GGCACAGCTGCTGATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCGG 120
 Db 61 GGCACAGCTGCTGATGCGAGATTTCACTACCTTTCTCTGTAATCTGTAAGTCCGG 120
 Qy 121 TTACAGATCCAAAGAGAAAGTGAAGGGGCGAGTGGCGGTACAGCCAGCGCCAGTACCG 180
 Db 121 CTGCAGATCCAAAGGAGAGTGAAGGGGCTAGTGGCGCACCGAGCCAGCGCCAGTACCG 180
 Qy 181 GGTGTGATGGGACCACTTCTGACCAATGTGCGTACTGAGGCCCCCGAAGCTTTACAAT 240
 Db 181 GGGTTCTGGTACCACTTCTGACCAATGTGCGCTGAGGCGCACTGAGGCTTCAACAT 240
 Qy 241 GGGCTGGTGGCGGCGCTGAGCGCCAAATGAGCTTTGCTCTGTCGCGCTGAT 300
 Db 241 GGGCTGGTGGCGGCGCTGAGCGCCAGATGAGCTTTGCTCTGTCGCGCTGAT 300
 Qy 301 GATTCTGTCAAACAGTTTACACCAAGGGCTCTGAGCATGCGCAATTTGGAGCCGCTC 360
 Db 301 GACTCTGTCAAACAGTTTACACCAAGGGCTCAGAGCATGAGGCAATGGAGCGCGCTC 360
 Qy 361 CTGACAGGACAGCCACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 361 CTGACAGGACAGCCACAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Qy 421 AAGTCCGATTCCAGCTGAGCGCGCGCTGAGAGTGTGAGAGATACCAAGACCGCTC 480
 Db 421 AAGTCCGCTTCCAGCTGAGCGCGCGCTGAGAGTGTGAGAGATACCAAGACCGCTC 480
 Qy 481 AATGCTTACAAAGCACTTCCCGGAGAGAGAGGTTCCGGGCTCTTGAAAGGAGCTCT 540
 Db 478 TCGAGCTTACAAAGCACTTCCCGGAGAGAGGTTCCGGGCTCTTGAAAGGAGCTCT 532
 Qy 541 CCCAATGTGCTGATATGCAATTTGCACTGTCTGAGCTGATGACTATGACTATC 600

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Db      533 -CCGATGTGCCCTTAATGCAATGTCACTGAGCTGTGACCTATGACCTCATC 591
Qy      601 AAGATGCGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTTCCACTTCACTT 660
Db      592 AAAGATCTCTCTGAA--GCCACCTCATGACAGATGACCTCCCTTCCACTTCACTT 648
Qy      661 GCCTTTGGGAGAGGCTTCTGACCACTGTACGCTCCCTTGAAGCTGTCAAGAG 720
Db      649 GCCTTGGGGGGGGGTTTGTGACCACTGTACGCTCCCTTGAAGTGTGATGATGAG 708
Qy      721 AGATACATGAATCTGCGCTTGGGCAAGTACAGTGGCTGGCACTGTGCGCTTACAG 780
Db      709 AGATACATGA--CTCTGCTGGGCGGAGTACCAAGCGGAGTCACTGTGCGCTTAC--A 762
Qy      781 CTCCAGAGAGAGGGGCGGAGGCTTCTACAAAGGTTCACTGCGCTTCTGCGCTT 840
Db      763 TGCTGGAGAGAGAGAGCCGCGCTTCTTCAACGAGGGGTTATGCTTCTTCTGCGCTT 822
Qy      841 GGTCTCTGGAACGTGTGATGTGTGTCACCTATGAGCACTGAAAGAGGCTTCACTGCT 900
Db      823 GGATCCTGGAACGTGTGATGTGTGTCACCTATGAGCACTTCAAGAGGCTTCACTGCT 882
Qy      901 GCGTGCACCTTCCCGAGAGGCTCCCTTCTGA 930
Db      883 GCTTACCAATCTCGGAGAGCACTTCTTCTGA 912

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RESULT 12

US-09-210-681-36
Sequence 36, Application US/09210681
Patent No. 6057109

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210.681
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 863-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-210-681-36

Query Match 66.5%; Score 618; DB 3; Length 1205;
Best Local Similarity 83.5%; Pred. No. 6,8e-158;
Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

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Qy      1 ATGGTTGGTTCAAGGCAAGATGAGGCGGCTTCTGACATGTGAAATTTCTTGGGCT 60
Db      1 ATGGTTGGTTCAAGGCAAGATGAGGCGGCTTCTGACATGTGAAATTTCTTGGGCT 60
Qy      61 GGCACAGCTGCTCTGATTCGAGATCTGATACCTTTCTCTGGATCTGCTAAATCCGG 120
Db      61 GGCACAGCTGCTCTGATTCGAGATCTGATACCTTTCTCTGGATCTGCTAAATCCGG 120
Qy      121 TTACAGATCCAGAGAAAGTCAAGGGGCGAGTGGCGCTACAGCCAGGCGCAATACCG 180
Db      121 CTGAGATCCAGAGAGAGAGTCAAGGGGCGAGTGGCGCTACAGCCAGGCGCAATACCG 180
Qy      181 GGTGTGATGGGACCACTTCTGACATGATGTGCTGATGAGGCGCCCGCAAGCTTCAAT 240
Db      181 GGTGTGATGGGACCACTTCTGACATGATGTGCTGATGAGGCGCCCGCAAGCTTCAAT 240
Qy      241 GGGCTGGTGGCGGCGCTGAGAGGCGCAATGAGCTTGGCTGTCCGATCGGCTGTAT 300
Db      241 GGGCTGGTGGCGGCGCTGAGAGGCGCAATGAGCTTGGCTGTCCGATCGGCTGTAT 300
Qy      301 GATTTGTCAAGAGTTCTTACCAAGAGGCTCTGAGCATGCGAGCATTTGGAGGCCCTC 360
Db      301 GATTTGTCAAGAGTTCTTACCAAGAGGCTCTGAGCATGCGAGCATTTGGAGGCCCTC 360
Qy      361 CTACAGAGGCAAGCAGAGGCTGCGTGGTGGCTGAGGCTGAGGCGGCGGAGGATGTGTA 420
Db      361 CTACAGAGGCAAGCAGAGGCTGCGTGGTGGCTGAGGCTGAGGCGGCGGAGGATGTGTA 420
Qy      421 AAGTTCGATTCAGAGCTCAAGGCGGCGTGGAGGTGTGAGGATTCAGAAAGGAGCTC 480
Db      421 AAGTTCGATTCAGAGCTCAAGGCGGCGTGGAGGTGTGAGGATTCAGAAAGGAGCTC 480
Qy      481 AATGCTTCAAGAGCAGTGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db      481 AATGCTTCAAGAGCAGTGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Qy      541 CCCAATGTGCTGATGATGCACTGATGCACTGATGCACTGATGCACTGATGCACTGATG 600
Db      541 CCCAATGTGCTGATGATGCACTGATGCACTGATGCACTGATGCACTGATGCACTGATG 600
Qy      601 AAGATGCGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTTCCACTTCACTT 660
Db      601 AAGATGCGCTCTCTGAAAGCCAACTCATGACAGATGACCTCCCTTCCACTTCACTT 660
Qy      661 GCCTTTGGGAGAGGCTTCTGACCACTGTACGCTCCCTTGAAGCTGTCAAGAG 720
Db      661 GCCTTTGGGAGAGGCTTCTGACCACTGTACGCTCCCTTGAAGCTGTCAAGAG 720
Qy      721 AGATACATGAATCTGCGCTTGGGCAAGTACAGTGGCTGGCACTGTGCGCTTACAG 780
Db      721 AGATACATGAATCTGCGCTTGGGCAAGTACAGTGGCTGGCACTGTGCGCTTACAG 780
Qy      781 CTCCAGAGAGAGGGGCGGAGGCTTCTACAAAGGTTCACTGCGCTTCTGCGCTT 840
Db      781 CTCCAGAGAGAGGGGCGGAGGCTTCTACAAAGGTTCACTGCGCTTCTGCGCTT 840
Qy      841 GGTCTCTGGAACGTGTGATGTGTGTCACCTATGAGCACTGAAAGAGGCTTCACTGCT 900
Db      841 GGTCTCTGGAACGTGTGATGTGTGTCACCTATGAGCACTGAAAGAGGCTTCACTGCT 900
Qy      901 GCGTGCACCTTCCCGAGAGGCTCCCTTCTGA 930
Db      901 GCGTGCACCTTCCCGAGAGGCTCCCTTCTGA 930
Qy      930 GCGTGCACCTTCCCGAGAGGCTCCCTTCTGA 960
Db      930 GCGTGCACCTTCCCGAGAGGCTCCCTTCTGA 960

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RESULT 13
US-08-946-719A-36
Sequence 36, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
NUMBER OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/234,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9030
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-946-719A-36

Query Match 66.5%; Score 618; DB 3; Length 1205;
Best Local Similarity 83.5%; Pred. No. 6,8e-158;
Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

QY 1 ATGCTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCGCATGTGAAGTTTCTGGGGCT 60
DB 1 ATGCTTGGGTTCAAGGCCACAGATGTGCCCCCAAGCCACTGTGAAGTTCTGGGGCT 60
QY 61 GGCACAGCTGCTGATCGCAGATCTCATCACTTTCTCTGATCTACTGATTAAGTCCGG 120
DB 61 GGCACAGCTGCTGATCGCAGATCTCATCACTTTCTCTGATCTACTGATTAAGTCCGG 120
QY 121 TTACAGATCCAAAGAGAAAGTCAAGGGCCAGTGGCCGCTACAGCCAGGCCAGTACCGC 180
DB 121 CTGCACATCCAAAGGGAGAGTCAAGGGCTAGTGGCCAGCCAGCCAGGCCAGTACCGT 180
QY 181 GGTGTATGGGACCACTTCTGACATGTGCGTACTGAGAGGCCGCCAGAGCCTTACAT 240
DB 181 GGGTCTGTGGTACCTCTTACATGATGTGGCCACTGAGGTCACAGAGCCTTACAT 240
QY 241 GGGCTGTGGCCGCTCGACAGGCCAAATGAGCTTGGCTCTGTGCGCATGGCCTGTAT 300

DB 241 GGGCTGTGGCCGCTCGACGCCCAAGATGAGCTTGGCTCTGTGCGCATGGCCTGTAC 300
QY 301 GATTCGTCAAAAGTTCTTACACCAAGGGCTTGAGCATGCCAGATTGGAGCCGCTC 360
DB 301 GATTCGTCAAAAGTTCTTACACCAAGGGCTTGAGCATGCCAGATTGGAGCCGCTC 360
QY 361 CTACAGAGCACACACAGGTGCCCTGCTGTGGCTGTGGCCAGCCAGATGTGTA 420
DB 361 CTGACAGGTGACACCAAGGTGCCCTGCTGTGGCTGTGGCCAGCTACAGATGTGTA 420
QY 421 AAGTCCGATTCACAGCTCAGGCCCGGGCTGAGGTGTGTGAGATACCAAGCAACCGTC 480
DB 421 AAGTCCGCTTCCAGGCTCCAGGCCCGGGCTGAGGTGTGTGAGATAC--AGAGACTG 477
QY 481 AATGCTTCAAAAGCAATTCGCCAGAGAGAAAGGTTCCGGGGCTCTGAGAAAGGACTCT 540
DB 478 TCGAGCTTCAAAAGCAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
QY 541 CCGAATGTGCTGCTAATGCTGATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 533 -CCGATGTGCTGCTAATGCTGATTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
QY 601 AAGATGCTCTCTGAGAAAGCCAACTTCATGACAGATGACTCTCTTCCACTTCACTTCT 660
DB 592 AAGATGCTCTCTGAGAAAGCCAACTTCATGACAGATGACTCTCTTCCACTTCACTTCT 648
QY 661 GCGTTTGGGGGAGGCTCTGACACACATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 649 GCGTTTGGGGGAGGCTCTGACACACATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 708
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DB 709 AGATACATGAA--CTGCTGCTGGGCAAGTACAGAGGCAAGTACATGTGCTCTTAC--A 762
QY 781 CTCCAGAAAGAGGGGGCCCCGAGCTCTTACAAAGGCTTATGCTGCTCTTCTCGGCTTG 840
DB 763 TGCTGGAG 822
QY 841 GATTCCTGAGACGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 823 GATTCCTGAGACGTGTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 882
QY 901 GCGTGCATCTCCGAGAGGCTCTCTTCTGA 930
DB 883 GCGTGCATCTCTGAGAGGCACTTCTGA 912

RESULT 14
US-09-547-983-36
Sequence 36, Application US/09547983
Patent No. 6518402
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,983
FILING DATE: 12-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/807,861
 FILING DATE: 26-FEB-1997
 APPLICATION NUMBER: US 08/518,878
 FILING DATE: 23-AUG-1995
 APPLICATION NUMBER: US 08/470,868
 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER: US 08/294,522
 FILING DATE: 23-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-066
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1205 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-09-547-983-36

Query Match 66.5%; Score 618; DB 4; Length 1205;
 Best Local Similarity 83.5%; Pred. No. 6.8e-158;
 Matches 777; Conservative 0; Mismatches 135; Indels 18; Gaps 6;

```

QY 1 ATGTTGGGTTCAAGGCGACAGATGTCCTCCCTGATGAGTTCTTGCGGCT 60
DB 1 ATGTTGGTTCAAGGCGACAGATGTCCTCCCTGATGAGTTCTTGCGGCT 60
QY 61 GGCACAGCTGCTGCATGCGATGTCATCACTTCTCTGATGATGTAAGTCCG 120
DB 61 GGCACAGCTGCTGCATGCGATGTCATCACTTCTCTGATGATGTAAGTCCG 120
QY 121 TTACGATCCAGAGAAAGTCAGGGGCGAGTGGCGCTACAGCCAGCCGCGTCC 180
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DB 181 GATGATGAGGACCATCTGACCATGATGTCGTAAGGAGCCCGGAGGCTCTAC 240
QY 181 GGCCTTCTGGGATCACTTCAACCATGATGTCGTAAGGAGCCCGGAGGCTCT 240
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QY 301 GATTCGTCAACCACTTCTACACCAAGGCTCTGAGATGCGACATTTGGAGCCGCTC 360
DB 301 GATTCGTCAACCACTTCTACACCAAGGCTCTGAGATGCGACATTTGGAGCCGCTC 360
QY 361 CTAGCAGGACGACCAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CTAGCAGGACGACCAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 361 CTAGCAGGACGACCAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 CTAGCAGGACGACCAAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 AAGTCCGATTCAGGCTCAGGCGGCGGCTGAGGTCGAGATACCAAGACCGCTC 480
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QY 421 AAGTCCGATTCAGGCTCAGGCGGCGGCTGAGGTCGAGATACCAAGACCGCTC 480
DB 421 AAGTCCGATTCAGGCTCAGGCGGCGGCTGAGGTCGAGATACCAAGACCGCTC 480
QY 481 AATGCTACAGACCATTTGCCGAGAGAGGCTTCCGGGCTCTCTGAGAGGAGCTCT 540
DB 481 AATGCTACAGACCATTTGCCGAGAGAGGCTTCCGGGCTCTCTGAGAGGAGCTCT 540
QY 478 TCGAGCTACAGAGACCATTTGCCGAGAGAGGCTTCCGGGCTCTCTGAGAGGAGCTCT 532
DB 478 TCGAGCTACAGAGACCATTTGCCGAGAGAGGCTTCCGGGCTCTCTGAGAGGAGCTCT 532
QY 541 CCCAATGTTGCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 600
DB 541 CCCAATGTTGCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 600
QY 533 -CCCAATGTTGCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 591
DB 533 -CCCAATGTTGCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 591
QY 601 AAGGATGCTCTCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 660
DB 601 AAGGATGCTCTCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 660
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DB 592 AAGGATGCTCTCTGTAAGGCTATGTAAGTGTGCTGTAAGTGTGTAAGTGTGTAAGTGTG 648
  
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QY 661 GCGTTGGGAGGAGCTTCTGACACATGTCATGCTCCCTCTGAGAGTGTCAAGC 720
 DB 649 GCGTTGGGAGGAGCTTCTGACACATGTCATGCTCCCTCTGAGAGTGTCAAGC 708
 QY 721 AGATACATGAACTTGCCTTGGGCGAGTACAGTACGCTGCGCACTGCTTACCATG 780
 DB 709 AGATACATGAACTTGCCTTGGGCGAGTACAGTACGCTGCGCACTGCTTACCATG 762
 QY 781 CTCGAGAGGAGGAGGCGGAGGCTTCTGACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 840
 DB 763 TCGTCCGAGAGGAGGAGGCGGAGGCTTCTGACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 822
 QY 841 GATTCCTGAGAGGAGGAGGCTTCTGACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 900
 DB 823 GATTCCTGAGAGGAGGAGGCTTCTGACAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 882
 QY 901 GCGTGCATCTCCGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTT 930
 DB 883 GCGTGCATCTCCGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTTCTGAGAGGCTT 912

RESULT 15
 US-09-702-705-1014
 Sequence 1014 Application US/09702705
 Patent No. 6504010
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Lodes, Michael A.
 APPLICANT: Fanger, Gary
 APPLICANT: Vedvick, Tom
 APPLICANT: Carter, Derrick
 APPLICANT: Retter, Marc
 APPLICANT: Mahlon, Jane
 APPLICANT: Fan, Liqun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121.478C14
 CURRENT FILING DATE: 2000-10-30
 NUMBER OF SEQ ID NOS: 1833
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1014
 LENGTH: 512
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-702-705-1014

Query Match 54.7%; Score 508.8; DB 4; Length 512;
 Best Local Similarity 99.6%; Pred. No. 1.8e-128;
 Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 GGGCGCGGAGGCTCTGACCAATGAGGCTGCTGCGGCTGCGAGCGGCAATAGAGCTTGC 60
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QY 339 TGGCAGATTTGGAGCGGCTCTCTAGAGGAGCAACAGAGGTCCTGCTGCTGCTGCT 398
DB 121 TGGCAGATTTGGAGCGGCTCTCTAGAGGAGCAACAGAGGTCCTGCTGCTGCTGCTGCT 180
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DB 241 TCGAGATACCAAGAGGAGGCTTGTGTAAGTTCGATTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 300
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Db	361	GCCGGGACCTATGACCTCATCAAGATGCCCTCTGAAAGCCAACTTCATGACAGATGA	420
QY	639	CCTCCCTTGCCACTTCACTTCTGCTTTGGGGGAGGCTTCTGCACTGATCATGCTTC	698
Db	421	CTCCCTTGCCACTTCACTTCTGCTTTGGGGGAGGCTTCTGCACTGATCATGCTTC	480
QY	699	CCCTGTAGACGTGTCAAGAGATACATGA	730
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Search completed: February 4, 2004, 20:09:33
 Job time : 77 secs

Fri Feb 6 16:59:29 2004

us-09-884-814-2.rmpb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 19:27:49 ; Search time 399 Seconds
(without alignments)

8585.911 Million cell updates/sec

Title: US-09-884-814-2

Perfect score: 930

Sequence: 1 atgtgttggttcgaagccac.....ccgagagctcccttcctga 930

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PTCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	100.0	930	US-09-884-814-2	Sequence 2, Appl1
2	930	100.0	930	US-10-265-689-2	Sequence 2, Appl1
3	930	100.0	1105	US-09-823-886A-3	Sequence 13, Appl1
4	930	100.0	1612	US-10-265-689-13	Sequence 13, Appl1
5	930	100.0	1643	US-10-240-965-183	Sequence 183, App
6	930	100.0	1646	US-10-159-563-344	Sequence 344, App
7	928.4	99.8	930	US-09-884-814-5	Sequence 5, Appl1
8	928.4	99.8	930	US-09-884-814-7	Sequence 7, Appl1
9	928.4	99.8	930	US-10-197-019-2	Sequence 2, Appl1
10	928.4	99.8	930	US-10-001-051B-1	Sequence 1, Appl1
11	880.4	94.7	960	US-09-567-856-1	Sequence 1, Appl1
12	762	81.9	1575	US-09-317-800A-1679	Sequence 1679, Ap
13	508.8	54.7	512	US-09-736-457-1014	Sequence 1014, Ap
14	508.8	54.7	512	US-09-902-941-1014	Sequence 1014, Ap
15	508.8	54.7	512	US-09-849-626-1014	Sequence 1014, Ap

16	508.8	54.7	512	US-10-113-872-1014	Sequence 1014, Ap
17	508.8	54.7	512	US-10-017-754-1014	Sequence 1014, Ap
18	474	51.0	1231	US-09-808-457-1	Sequence 1, Appl1
19	472.4	50.8	1192	US-09-734-134-1	Sequence 1, Appl1
20	472.4	50.8	1192	US-09-826-507-1	Sequence 1, Appl1
21	447.2	47.5	1175	US-10-062-674-1405	Sequence 1405, Ap
22	411	44.2	1132	US-09-808-457-3	Sequence 3, Appl1
23	411	44.2	1132	US-09-823-886A-5	Sequence 5, Appl1
24	316.4	34.0	318	US-09-136-457-1376	Sequence 1376, Ap
25	316.4	34.0	318	US-09-902-941-1376	Sequence 1376, Ap
26	316.4	34.0	318	US-09-849-626-1376	Sequence 1376, Ap
27	316.4	34.0	318	US-10-113-872-1376	Sequence 1376, Ap
28	316.4	34.0	318	US-10-017-754-1376	Sequence 1376, Ap
29	297	31.9	924	US-09-823-886A-1	Sequence 1, Appl1
30	286.8	30.8	290	US-10-101-510-323	Sequence 323, App
31	247.2	26.6	764	US-09-910-943-628	Sequence 628, App
32	216.8	23.3	1631	US-10-265-689-10	Sequence 10, Appl1
33	216.8	23.3	7578	US-10-265-689-29	Sequence 29, Appl1
34	216.4	23.3	9314	US-10-197-019-1	Sequence 1, Appl1
35	188	20.2	556	US-10-027-632-134303	Sequence 134303, Ap
36	188	20.2	556	US-10-027-632-134304	Sequence 134304, Ap
37	188	20.2	556	US-10-027-632-134303	Sequence 134303, Ap
38	188	20.2	556	US-10-027-632-134304	Sequence 134304, Ap
39	179	19.2	9246	US-10-265-689-25	Sequence 25, Appl1
40	178.6	19.2	847	US-09-724-134-5	Sequence 5, Appl1
41	176	18.9	1592	US-10-265-689-12	Sequence 12, Appl1
42	166.6	17.9	416	US-09-960-352-3287	Sequence 3287, Ap
43	159.4	17.1	717	US-10-265-689-11	Sequence 11, Appl1
44	153	16.5	921	US-09-938-842A-761	Sequence 761, App
45	153	16.5	921	US-09-938-842A-761	Sequence 761, App

ALIGNMENTS

RESULT 1
US-09-884-814-2
Sequence 2, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chen, Jin-Long
APPLICANT: Amarel, M. Catherine
TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
FILE REFERENCE: 018781-001110US
CURRENT APPLICATION NUMBER: US/09/884, 814
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 09/124,293
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
US-09-884-814-2

Query Match 100.0%; Score 930; DB 10; Length 930;

Best Local Similarity 100.0%; Pred. No. 1,1e-281; Indels 0; Gaps 0;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GGCAGAGCTGCTGATGCAAGATGTCATGCTTCTTGATGCTGAAGTCCGG	120
DB	61	GGCAGAGCTGCTGATGCAAGATGTCATGCTTCTTGATGCTGAAGTCCGG	120

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Db 121 TTACAGATCCAGAGAGAAAGTCAAGGGGCGAGTGGCGCTACAGCCGAGCGCCAGTACCGC 180
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QY 421 AAGTCCGATTCGAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 480
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; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-265-689-2

Query Match 100.0%; Score 930; DB 15; Length 930;
Best Local Similarity 100.0%; Pred. No. 1,1e-281;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGGTTCAAGGCGACAGATGAGCCCTTACTGACATGTGAATTTCTTGGGACT 60
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QY 61 GGCACAGCTGCTGACATGCGAGATCTATACCTTTCTTGTGATATCTGTAAGTCCG 120
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QY 481 AATGCTTCAAGACCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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RESULT 2
US-10-265-689-2
; Sequence 2: Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLEMAN, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICOUIER, DANIEL
; APPLICANT: BOUTILAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08

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; SEQ ID NO 183
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 093687.6
US-10-240-965-183

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Best Local Similarity 100.0%; Pred. No. 1,36-281;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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733  CTAGAGAGGCAAGCAAGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 792
421  AAGTCCGATTTCAAGCTCAAGGCTCGGCGCTGAGAGTGTGAGATACCAAGCAACGCTC 480
793  AAGTCCGATTTCAAGCTCAAGGCTCGGCGCTGAGAGTGTGAGATACCAAGCAACGCTC 852
481  AATGCCATCAAGACATTTGCCGAGAGAGAGGTTCCGGGGCTCTGGAAGAGGACCTCT 540
853  AATGCCATCAAGACATTTGCCGAGAGAGAGGTTCCGGGGCTCTGGAAGAGGACCTCT 912
541  CCCAATGTTCTGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 600
913  CCCAATGTTCTGTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 972
601  AAGATGCTCTCTGTAAGGCACTTCAATGACAGATGACCTCCCTTGGCACTTCACTCT 660
973  AAGATGCTCTCTGTAAGGCACTTCAATGACAGATGACCTCCCTTGGCACTTCACTCT 1032
1033  GCTTTGGGCGAGGCTTCTGCAACATGTCATGCTCCCTCTGTAAGAGTGTGCAAGAG 1092
721  AGATPACATGAATCTGCTGCTGGGCGAGTACAGTACGCTGGGCGACCTGTCACAGT 780
1093  AGATPACATGAATCTGCTGCTGGGCGAGTACAGTACGCTGGGCGACCTGTCACAGT 1152
781  CTCAGAGAGAGGAGGCGCCGAGGCTTCTCAAGAGGTTATGAGGCTCTTCTCGCGTTG 840
1153  CTCAGAGAGAGGAGGCGCCGAGGCTTCTCAAGAGGTTATGAGGCTCTTCTCGCGTTG 1212
841  GGTTCCTGGAACGTGTGATGTTGCTCACTTACAGAGTGAAGAGGCTCTCATGGCT 900
1213  GGTTCCTGGAACGTGTGATGTTGCTCACTTACAGAGTGAAGAGGCTCTCATGGCT 1272

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; RESULT 5
; US-10-240-965-183
; Sequence 183, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAMN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program

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QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 DB 1273 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 1302

RESULT 6

US-10-159-563-344
 / Sequence 344, Application US/10159563
 / Publication No. US20040009154A1
 / GENERAL INFORMATION:
 / APPLICANT: Khan, Javed
 / APPLICANT: Ringer, Markus
 / APPLICANT: Peterson, Carsten
 / APPLICANT: Melzer, Paul
 / TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
 / TITLE OF INVENTION: DIAGNOSIS AND FOR TREATING THE THERAPY OF SELECT CANCERS
 / FILE REFERENCE: 11613.56US11
 / CURRENT APPLICATION NUMBER: US/10/159,563
 / PRIOR FILING DATE: 2002-12-09
 / PRIOR FILING DATE: 2002-04-25
 / NUMBER OF SEQ ID NOS: 444
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 344
 / LENGTH: 1646
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 US-10-159-563-344

Query Match 100.0%; Score 930; DB 12; Length 1646;
 Best Local Similarity 100.0%; Pred. No. 1.3e-281;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGCACAGATGCGCCCTACTGCGACGTGAAGTTCTTGGGCT 60
 DB 381 ATGGTTGGGTTCAAGGCGCACAGATGCGCCCTACTGCGACGTGAAGTTCTTGGGCT 440
 QY 61 GGCACAGCTGCTGCATCGCAGATCTCATACCTTCTCTTGATCTGCTAAAGTCCGG 120
 DB 441 GGCACAGCTGCTGCATCGCAGATCTCATACCTTCTCTTGATCTGCTAAAGTCCGG 500
 QY 121 TTACAGATCCAGAGAAAGTGAAGGCGCGAGTGCAGTACAGGCGCCAGTACCGC 180
 DB 501 TTACAGATCCAGAGAAAGTGAAGGCGCGAGTGCAGTACAGGCGCCAGTACCGC 560
 QY 181 GGTGTGATGAGGACCAATTTGACCATGTGCTGACTGAAGGCGCCGAAAGCTTTACAT 240
 DB 561 GGTGTGATGAGGACCAATTTGACCATGTGCTGACTGAAGGCGCCGAAAGCTTTACAT 620
 QY 241 GGGCTGTGCGCGGCTGAGAGGCGCAATGAGCTTGTGCTGTGCGGATGCGGCTGAT 300
 DB 621 GGGCTGTGCGCGGCTGAGAGGCGCAATGAGCTTGTGCTGTGCGGATGCGGCTGAT 680
 QY 301 GATTCTGTCAACAGTTCTTACACCAAGGCGCTTGAAGCATGCCAGATTGGAGCGGCTC 360
 DB 681 GATTCTGTCAACAGTTCTTACACCAAGGCGCTTGAAGCATGCCAGATTGGAGCGGCTC 740
 QY 361 CTAGCAGGAGGAGCCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 741 CTAGCAGGAGGAGCCACAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
 QY 421 AAGGTCGATTCAGAGCTAGGCGCGGCTGAGAGTGTGAGAGTACCAAGCACCGCTC 480
 DB 801 AAGGTCGATTCAGAGCTAGGCGCGGCTGAGAGTGTGAGAGTACCAAGCACCGCTC 860
 QY 481 AATGCTTCAAGACCAATTTGCGGAGAGAGAGGTTCCGGGCGCTTGAAGAGGAGCTCT 540
 DB 861 AATGCTTCAAGACCAATTTGCGGAGAGAGAGGTTCCGGGCGCTTGAAGAGGAGCTCT 920
 QY 541 CCAATGTTGCTGTAATGCAATTTCACTGTGCTGAGCTGTAAGCTTATGACCTCATC 600
 DB 921 CCAATGTTGCTGTAATGCAATTTCACTGTGCTGAGCTGTAAGCTTATGACCTCATC 980

QY 601 AAGATGCCCTCTCGAAGGCAAGCTTATGACAGATGAGCTCCCTTCCACTTCACTTCT 660
 DB 981 AAGATGCCCTCTCGAAGGCAAGCTTATGACAGATGAGCTCCCTTCCACTTCACTTCT 1040
 QY 661 GCCTTTGGGCGAGGCTTCTGACACCACTGTGATGCGCTCCCTGTAGAGGTGTGCAAGAG 720
 DB 1041 GCCTTTGGGCGAGGCTTCTGACACCACTGTGATGCGCTCCCTGTAGAGGTGTGCAAGAG 1100
 QY 721 AGATTCATGAACTTGTGCGCTGCGGAGTACAGTATGAGGCGGCGAGTGTGCTTACAG 780
 DB 1101 AGATTCATGAACTTGTGCGCTGCGGAGTACAGTATGAGGCGGCGAGTGTGCTTACAG 1160
 QY 781 CTCGAGAGAGAGGCGCGCGCGCTTCTTACAAAGGTTCAATGCGCTCTTCTCGCGCTG 840
 DB 1161 CTCGAGAGAGAGGCGCGCGCGCTTCTTACAAAGGTTCAATGCGCTCTTCTCGCGCTG 1220
 QY 841 GGTTCCTGGAACGTGTGATGTTGTGTACCTTATGAGAGTGAAGAGCCCTCATGCGCT 900
 DB 1221 GGTTCCTGGAACGTGTGATGTTGTGTACCTTATGAGAGTGAAGAGCCCTCATGCGCT 1280
 QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 DB 1281 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 1310

RESULT 7

US-09-884-814-5
 / Sequence 5, Application US/09884814
 / Patent No. US20020127600A1
 / GENERAL INFORMATION:
 / APPLICANT: Chen, Jin-Jong
 / APPLICANT: Amaral, W. Catherine
 / APPLICANT: Tularik Inc.
 / TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
 / TITLE OF INVENTION: Methods of Use
 / FILE REFERENCE: 018781-001110US
 / CURRENT APPLICATION NUMBER: US/09/884,814
 / PRIOR FILING DATE: 2001-06-18
 / PRIOR FILING DATE: 1998-07-29
 / NUMBER OF SEQ ID NOS: 8
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 5
 / LENGTH: 930
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)..(930)
 / OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tarragila et al.
 US-09-884-814-5

Query Match 99.8%; Score 928.4; DB 10; Length 930;
 Best Local Similarity 99.9%; Pred. No. 3.6e-281;
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGCACAGATGCGCCCTACTGCGACGTGAAGTTCTTGGGCT 60
 DB 1 ATGGTTGGGTTCAAGGCGCACAGATGCGCCCTACTGCGACGTGAAGTTCTTGGGCT 60
 QY 61 GGCACAGCTGCTGCATCGCAGATCTCATACCTTCTCTGATGATGTGTAAGTCCGG 120
 DB 61 GGCACAGCTGCTGCATCGCAGATCTCATACCTTCTCTGATGATGTGTAAGTCCGG 120
 QY 121 TTACAGATCCAGAGAAAGTCAAGGCGCGAGTGCAGTACAGGCGCCAGTACCGC 180
 DB 121 TTACAGATCCAGAGAAAGTCAAGGCGCGAGTGCAGTACAGGCGCCAGTACCGC 180
 QY 181 GGTGTGATGAGGACCAATTTGACCATGTGCTGACTGAAGGCGCCGGAAGCTTTACAT 240
 DB 181 GGTGTGATGAGGACCAATTTGACCATGTGCTGACTGAAGGCGCCGGAAGCTTTACAT 240
 QY 241 GGGCTGTGCGCGGCTGAGAGGCGCAATGAGCTTGTGCTGTGCGGATGCGGCTGAT 300

Db 241 GGGCTGGTTGCGCGCCGCGCAAGAGTTGGCTTGTCTGTCGAGTGGCTGTAT 300
Qy 301 GATTTCGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Db 301 GATTTCGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Qy 361 CTAGCAGGACGACCAAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 361 CTAGCAGGACGACCAAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
Db 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
Qy 481 AATGCTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGCGCTCTGAAAAGGACCTCT 540
Db 481 AATGCTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGCGCTCTGAAAAGGACCTCT 540
Qy 541 CCCAATGTTGCTGTAATGCCATTGTCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 CCCAATGTTGCTGTAATGCCATTGTCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 601 AAGATGCGCTCCGAAAGCAACCTCATGACAGATGACCTCCCTTGCACCTTCTCT 660
Db 601 AAGATGCGCTCCGAAAGCAACCTCATGACAGATGACCTCCCTTGCACCTTCTCT 660
Qy 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 AGATACATGAATCTGTGCTGTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 721 AGATACATGAATCTGTGCTGTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Qy 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTTCTTCTCCGCTTG 840
Db 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTTCTTCTCCGCTTG 840
Qy 841 GGTTCCTGGAACGT 900
Db 841 GGTTCCTGGAACGT 900
Qy 901 GCGTGCATTCGCCGAGAGGCTCCCTTCTGA 930
Db 901 GCGTGCATTCGCCGAGAGGCTCCCTTCTGA 930

RESULT 8

US-09-884-814-7
Sequence 7, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chem. Jin-Long
APPLICANT: Amaral, M. Catherine
APPLICANT: Tularik Inc.
TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
FILE REFERENCE: 018781-00110US
CURRENT APPLICATION NUMBER: US/09/884,814
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 09/124,293
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 7
LENGTH: 930
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(930)
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.

US-09-884-814-7
Query Match 99.8%; Score 928.4; DB 10; Length 930;
Best Local Similarity 99.9%; Pred. 3.6e-281;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTTGGTTCAAGGCCACAGATGTGCCCCCTTACTGCACTGTGAAAGTTCTTTGGGCT 60
Db 1 ATGTTGGTTCAAGGCCACAGATGTGCCCCCTTACTGCACTGTGAAAGTTCTTTGGGCT 60
Qy 61 GGCACAGCTGCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 120
Db 61 GGCACAGCTGCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 120
Qy 121 TTACAGATCAAGAGAAAGTCAAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 180
Db 121 TTACAGATCAAGAGAAAGTCAAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 180
Qy 181 GGTGTGATGGGACCAATCTGACATGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGT 240
Db 181 GGTGTGATGGGACCAATCTGACATGAGTGTGCTGAGTGTGAGTGTGAGTGTGAGT 240
Qy 241 GGGCTGTTGCGGCTGAGGCGCAATGAGCTTTGCTTGTCCGATTCGCTGTAT 300
Db 241 GGGCTGTTGCGGCTGAGGCGCAATGAGCTTTGCTTGTCCGATTCGCTGTAT 300
Qy 301 GATTTCGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Db 301 GATTTCGTCAACAGTTCTACACCAAGGCTCTGACATGCCAGATTTGGAGCCGCTC 360
Qy 361 CTAGCAGGACGACCAAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 361 CTAGCAGGACGACCAAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
Db 421 AAGTCCGATTCCAGCTCAGGCGCGGCTGAGGCTGTGAGATACCAAGACCGCTC 480
Qy 481 AATGCTCAAGACCATTTGCCGAGAGAGGTTCCGGGCGCTCTGAAAAGGACCTCT 540
Db 481 AATGCTCAAGACCATTTGCCGAGAGAGGTTCCGGGCGCTCTGAAAAGGACCTCT 540
Qy 541 CCCAATGTTGCTGTAATGCCATTGTCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 CCCAATGTTGCTGTAATGCCATTGTCACTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 601 AAGATGCGCTCCGAAAGCAACCTCATGACAGATGACCTCCCTTGCACCTTCTCT 660
Db 601 AAGATGCGCTCCGAAAGCAACCTCATGACAGATGACCTCCCTTGCACCTTCTCT 660
Qy 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 GCGTTGGGGGAGGCTTCTGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 AGATACATGAATCTGTGCTGTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 721 AGATACATGAATCTGTGCTGTGAGCACTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Qy 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTTCTTCTCCGCTTG 840
Db 781 CTCCAGAGAGAGGAGGCGCCGAGGCTTCTACAAAGGTTCAAGGCTTCTTCTCCGCTTG 840
Qy 841 GGTTCCTGGAACGT 900
Db 841 GGTTCCTGGAACGT 900
Qy 901 GCGTGCATTCGCCGAGAGGCTCCCTTCTGA 930
Db 901 GCGTGCATTCGCCGAGAGGCTCCCTTCTGA 930

RESULT 9

US-10-197-019-2

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; Sequence 2, Application US/10197019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
; APPLICANT: Denton, R. Rex
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent version 3.1
; SEQ ID NO: 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-197-019-2

Query Match      99.8%; Score 928.4; DB 13; Length 930;
Best Local Similarity 99.9%; Pred. No. 3.6e-281;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGACAGATGTGCGCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 60
DB 1 ATGGTTGGGTTCAAGGCGACAGATGTGCGCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 60
QY 61 GGCACAGCTGCGCTGCATGCGAGATCTATCACTTTCTCTGTACTGCTTAAAGTCGG 120
DB 61 GGCACAGCTGCGCTGCATGCGAGATCTATCACTTTCTCTGTACTGCTTAAAGTCGG 120
QY 121 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
DB 121 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
QY 122 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
DB 122 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
QY 181 GGTGTGATGGGACCATCTGACATGTGTGCTACTGAGCGGCCCGAGACCTCTACAAAT 240
DB 181 GGTGTGATGGGACCATCTGACATGTGTGCTACTGAGCGGCCCGAGACCTCTACAAAT 240
QY 241 GGGCTGTGTCGGGCGCTGCAAGGCCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
DB 241 GGGCTGTGTCGGGCGCTGCAAGGCCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
QY 241 GGGCTGTGTCGGGCGCTGCAAGGCCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
DB 241 GGGCTGTGTCGGGCGCTGCAAGGCCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
QY 301 GATTCGTCAACAAGTTCTACACCAAGGAGCTCTGAGCATGCGACATTTGGGAGCGGCTC 360
DB 301 GATTCGTCAACAAGTTCTACACCAAGGAGCTCTGAGCATGCGACATTTGGGAGCGGCTC 360
QY 361 CTAGCAGGCGACCAACAGAGTGCCTGCTGTGCTGTGCGCCAGCCCAAGATGTGTA 420
DB 361 CTAGCAGGCGACCAACAGAGTGCCTGCTGTGCTGTGCGCCAGCCCAAGATGTGTA 420
QY 421 AAGGTCGATTCGAAGCTCAGGCGCGGCTGAGAGTGTGCGGAATACCAAGACCGTC 480
DB 421 AAGGTCGATTCGAAGCTCAGGCGCGGCTGAGAGTGTGCGGAATACCAAGACCGTC 480
QY 481 AATGCTTCAACAAGCAATTCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 481 AATGCTTCAACAAGCAATTCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 CCCAATGTGCTGTAAGGCAATTCGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTATC 600
DB 541 CCCAATGTGCTGTAAGGCAATTCGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTATC 600
QY 601 AAGGATGCGCTCTGTAAGGCAATTCGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTATC 660
DB 601 AAGGATGCGCTCTGTAAGGCAATTCGCACTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTATC 660
QY 661 GCGTTTGGGCGAGGCTTTCGACCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTG 720
DB 661 GCGTTTGGGCGAGGCTTTCGACCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTG 720

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QY 721 AGATCACTGACTTGTGCTGCGGCGACGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 721 AGATCACTGACTTGTGCTGCGGCGACGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 CTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
DB 781 CTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 GGTTCCTGGAACGTGTGATGTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACT 900
DB 841 GGTTCCTGGAACGTGTGATGTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACTGTGCACT 900
QY 901 GCGTCACTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 GCGTCACTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960

RESULT 10
US-10-001-051B-1
; Sequence 1, Application US/10001051B
; Publication No. US20020172958A1
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Wilella
; APPLICANT: Shamloo, Mehdiad
; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Waloeh, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: Agi Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
; TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
; FILE REFERENCE: 019488-003010US
; CURRENT APPLICATION NUMBER: US/10/001,051B
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
; US-10-001-051B-1

Query Match      99.8%; Score 928.4; DB 14; Length 930;
Best Local Similarity 99.9%; Pred. No. 3.6e-281;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGACAGATGTGCGCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 60
DB 1 ATGGTTGGGTTCAAGGCGACAGATGTGCGCCCTACTGCGACTGTGAAGTTTCTTGGGGCT 60
QY 61 GGCACAGCTGCGCTGCATGCGAGATCTATCACTTTCTCTGTACTGCTTAAAGTCGG 120
DB 61 GGCACAGCTGCGCTGCATGCGAGATCTATCACTTTCTCTGTACTGCTTAAAGTCGG 120
QY 121 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
DB 121 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
QY 121 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
DB 121 TTACAGATCCAAAGGAGAAAGTCAGGGGCGAGTGGGGCTACAGCGAGCGCCAGTACCG 180
QY 181 GGTGTGATGGGACCATCTGACATGTGTGCTACTGAGCGGCCCGAGACCTCTACAAAT 240
DB 181 GGTGTGATGGGACCATCTGACATGTGTGCTACTGAGCGGCCCGAGACCTCTACAAAT 240
QY 241 GGGCTGTGTCGGGCGCTGCAAGGCCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
DB 241 GGGCTGTGTCGGGCGCTGCAAGGCCAATGAGCTTTGCTGTGCCCATGCGCTGTAT 300
QY 301 GATTCGTCAACAAGTTCTACACCAAGGAGCTCTGAGCATGCGACATTTGGGAGCGGCTC 360

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APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling
 FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US/09/917, 800A
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/222,580
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/230,029
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/230,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/232,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/235,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/237,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/238,884
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1679
 LENGTH: 1575
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 FEATURE:
 OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_019354
 US-09-917-800A-1679

Query Match 81.3%; Score 762; DB 10; Length 1575;
 Best Local Similarity 88.7%; Pred. No. 7,9e-229;
 Matches 825; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 ATGTTGGGTTCAAGGCCCAAGATGTGCTCCCTACTGACCTGTGAAGTTCTTGGGGCT 60
 DB 345 ATGTTGGTTCAGAGGCCACGATGTGCTCCCTCAAGCCACCTGGAAGTTCTGGGGCT 404
 QY 61 GGCACAGCTGCTCATCGAGATCTCATCACTTCTCTGATACCTGTAAGTCCGG 120
 DB 405 GGCACAGAGCTGATGTGAGATCTCATCACTTCTCTGATACCTGTAAGTCCGG 464
 QY 121 TTACAGATCCAAAGAAAGTCAAGGGGCACTGGGCTACAGCCAGCCGCTACCCG 180
 DB 465 CTGAGATCCAAAGGAGAGTCAAGGGGCACTGGGCTACAGCCGCTACCCG 524
 QY 181 GATGATGGGCACTTCTGACCATGTGCTGCTAGAGGAGCCCGGAACTCTACAT 240
 DB 525 GGCCTGTGGGCACTTCTGACCATGTGCTGCTAGAGGAGCCCGGAACTCTACAT 584
 QY 241 GGGCTGTGGGCTGCGGCTGCAAGCCCAATGAGCTTTCCTGTGCTGCGCATGCGCTGTAT 300
 DB 585 GGGCTGTGCGCGGCTGCAAGCCCAATGAGCTTTCCTGTGCTGCGCATGCGCTGTAT 644
 QY 301 GATTTGTCAAAAGATTTTCAACCAAGGCTCTAGAGATGCGACATTTGGAGCCGCTC 360
 DB 645 GATCTGTAAAGCAATTTTCAACCAAGGCTCTAGAGATGCGACATTTGGAGCCGCTC 704
 QY 361 CTAGCAGGAGCACCACAGTGCCTGTGCTGTGCTGTGCGCCAGCCACGAGATGTGTA 420
 DB 705 CTGCGAGGAGCACCACAGTGCCTGTGCTGTGCTGTGCGCCACCTTACAGATGTGTA 764
 QY 421 AAGGTCCATTTCAAGCTCAGGCTCGGGCTGAGGTGTGGAATACCAAGACCGTC 480
 DB 765 AAGGTCCGCTTCAAGCCCAAGGCTCGGGCTGAGGTGTGGAATACCAAGACCGTC 824
 QY 481 AATGCTTCAAGACCATTTGCTCCGAGAGAGAGGTTCCGGGCTCTTGAAAAGGACCTCT 540
 DB 825 GAAGCTTCAAGACCATTTGCAAGAGAGAGGATCCGGGCTCTTGAAAAGGACCTCT 884

QY 541 CCCAATGTTGCTGTAAATGCCAATGTCAACTGTGTAGTGTGACCTATGACCTCATC 600
 DB 885 CCCAATGTTGCCGAATATCCATGTCAACTGTGTAGTGTGACCTATGACCTCATC 944
 QY 601 AAGAGTCCCTCTGAAAGCCCACTCAAGTACAGTACCTCCCTGCACTTCACTCT 660
 DB 945 AAGATATCTCTTAAAGCCCACTCAAGTACAGTACCTCCCTGCACTTCACTCT 1004
 QY 661 GCCTTGGGGCAGCTTGTGACCACTGTCAATGCTTCCCTGTAGACGTGTCAAGC 720
 DB 1005 GCCTTGGGGCAGCTTGTGACCACTGTCAATGCTTCCCTGTAGACGTGTCAAGC 1064
 QY 721 AGATATATATCTGTGCTGCTGAGGAGTACCTGTGCTGCTGCTGCTGCTGCTG 780
 DB 1065 AGATATATATCTGTGCTGCTGAGGAGTACCTGTGCTGCTGCTGCTGCTGCTG 1124
 QY 781 CTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 1125 CTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1184
 QY 841 GATTCCTGAACGTGTGATGTTCTGCTACCTATAGAGCTGAAACGAGCCCTATGCT 900
 DB 1185 GATTCCTGAACGTGTGATGTTCTGCTACCTATAGAGCTGAAACGAGCCCTATGCT 1244
 QY 901 GCCTGCACTCCCGAGAGGCTCCCTTCTGA 930
 DB 1245 GCCTATGATCCCGAGAGGACCTTTTGA 1274

RESULT 13

US-09-736-457-1014
 Sequence 1014, Application US/09736457
 Patent No. US20020168637A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Bangur, Chaitanya S.
 APPLICANT: Lodes, Gary
 APPLICANT: Vedvick, Tom
 APPLICANT: Carter, Darrick
 APPLICANT: Retter, Marc
 APPLICANT: Mannion, Jane
 APPLICANT: Fan, Liqun
 APPLICANT: Wang, Aijun
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 FILE REFERENCE: 210121, 478C15
 CURRENT APPLICATION NUMBER: US/09/736,457
 CURRENT FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 1864
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1014
 LENGTH: 512
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-736-457-1014

Query Match 54.7%; Score 508.8; DB 10; Length 512;
 Best Local Similarity 39.6%; Pred. No. 2e-149;
 Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 219 GGGCCCCGGAAGCTCTACAAATGGGCTGTGCGGGCTGCAAGCCGCAATAGGCTTTC 278
 DB 1 GGGCCCCGGAAGCTCTACAAATGGGCTGTGCGGGCTGCAAGCCGCAATAGGCTTTC 60
 QY 279 CTGTGTGCGATCGGCTGTATATCTGTCAAAAGTTCTACCAAGGAGGCTGTAGCA 338
 DB 61 CTGTGTGCGATCGGCTGTATATCTGTCAAAAGTTCTACCAAGGAGGCTGTAGCA 120
 QY 339 TGCAGCATTTGGAGCCGCTTCTTACAGGCAACACAGAGTGCCTGCTGCTGCTGCT 398
 DB 121 TGCAGCATTTGGAGCCGCTTCTTACAGGCAACACAGAGTGCCTGCTGCTGCTGCT 180

QY 399 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAAGCTCAGCCGCGGCTGAGAGTGG 458
DB 181 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAAGCTCAGCCGCGGCTGAGAGTGG 240
QY 459 TCGGAGATACCAAGACCGTCAATGCTCAAGACCAATTCGCGAGAGAGGTTCCG 518
DB 241 TCGGAGATACCAAGACCGTCAATGCTCAAGACCAATTCGCGAGAGAGGTTCCG 300
QY 519 GGACCTCTGGAAGAGGACCTCTCCCATGTTGCTGATATGCTCAATGCTCAATGCTGTA 578
DB 301 GGACCTCTGGAAGAGGACCTCTCCCATGTTGCTGATATGCTCAATGCTCAATGCTGTA 360
QY 579 GCTGTGACCTATGACCTCTCAAGAGTCCCTCTGGAAGAGGACCTCTCAAGAGTGA 638
DB 361 GCGGCGACCTATGACCTCTCAAGAGTCCCTCTGGAAGAGGACCTCTCAAGAGTGA 420
QY 639 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGTCATGCGCTC 698
DB 421 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGTCATGCGCTC 480
QY 699 CCTGTAGACGTGTCAAGAGATACATGA 730
DB 481 CCTGTAGACGTGTCAAGAGATACATGA 512

RESULT 14
US-09-902-941-1014
; Sequence 1014, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Maranabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvik, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-902-941-1014

Query Match 54.7%; Score 508.8; DB 10; Length 512;
Best Local Similarity 99.6%; Pred. No. 2e-149; 2; Indels 0; Gaps 0;
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 219 GGCCCCCGAAGCTCTTACAAATGGGCTGTGTGCGGCTTGCAGCGCCAAATGAGCTTTGC 278
DB 1 GGCCCCCGAAGCTCTTACAAATGGGCTGTGTGCGGCTTGCAGCGCCAAATGAGCTTTGC 60
QY 279 CTGTGTCGCGATGGGCGGCTGTATGATTTCTGCAAAAGTTCTACCAAGAGGCTCTGAGCA 338
DB 61 CTGTGTCGCGATGGGCGGCTGTATGATTTCTGCAAAAGTTCTACCAAGAGGCTCTGAGCA 120
QY 339 TGCAGACATTGGAGCGGCTCTTACAGGCGAGCACCAAGGTGCTGCTGTGCTGT 398
DB 121 TGCAGACATTGGAGCGGCTCTTACAGGCGAGCACCAAGGTGCTGCTGTGCTGT 180
QY 399 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAAGCTCAGCCGCGGCTGAGAGTGG 458
DB 181 GGCCCAAGCCCAAGATGTGTAAAGTTCGATTCAAGCTCAGCCGCGGCTGAGAGTGG 240

QY 459 TCGGAGATACCAAGACCGTCAATGCTCAAGACCAATTCGCGAGAGAGGTTCCG 518
DB 241 TCGGAGATACCAAGACCGTCAATGCTCAAGACCAATTCGCGAGAGAGGTTCCG 300
QY 519 GGACCTCTGGAAGAGGACCTCTCCCATGTTGCTGATATGCTCAATGCTCAATGCTGTA 578
DB 301 GGACCTCTGGAAGAGGACCTCTCCCATGTTGCTGATATGCTCAATGCTCAATGCTGTA 360
QY 579 GCTGTGACCTATGACCTCTCAAGAGTCCCTCTGGAAGAGGACCTCTCAAGAGTGA 638
DB 361 GCGGCGACCTATGACCTCTCAAGAGTCCCTCTGGAAGAGGACCTCTCAAGAGTGA 420
QY 639 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGTCATGCGCTC 698
DB 421 CCTCCCTTGCACCTTCACTTCTGCTTGGGCGAGGCTTCTGACCACTGTCATGCGCTC 480
QY 699 CCTGTAGACGTGTCAAGAGATACATGA 730
DB 481 CCTGTAGACGTGTCAAGAGATACATGA 512

RESULT 15
US-09-849-626-1014
; Sequence 1014, Application US/09849626
; Publication No. US20020197699A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tonglong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1014
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-626-1014

Query Match 54.7%; Score 508.8; DB 10; Length 512;
Best Local Similarity 99.6%; Pred. No. 2e-149; 2; Indels 0; Gaps 0;
Matches 510; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 61 CTGTGTCGCGATGGGCGGCTGTATGATTTCTGCAAAAGTTCTACCAAGAGGCTCTGAGCA 120
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QY 459 TCGGAGATACCAAGACCGTCAATGCTCAAGACCAATTCGCGAGAGAGGTTCCG 518
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Qy	639	CCTGCTTGGCACTTCACTTGTGCTTGGGGGAGGCTTCTGACACCACTGTCAATGGCTTC	698
Db	421	CCTGCTTGGCACTTCACTTGTGCTTGGGGGAGGCTTCTGACACCACTGTCAATGGCTTC	480
Qy	699	CCCTGTAGACGTGTCAAGACGATACATGA	730
Db	481	CCCTGTAGACGTGTGTCAAGACGATACATGA	512

Search completed: February 4, 2004, 21:21:56
 Job time : 401 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 18:26:09 ; Search time 3498 Seconds
(without alignments)
8817.128 Million cell updates/sec

Title: US-09-884-814-2

Perfect score: 930
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 333688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Result No.	Score	Query Match	Length	DB ID	Description
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2	930	100.0	930	1	PCT-US99-17246-1
3	930	100.0	930	2	PCT-US99-06317-2
4	930	100.0	930	2	PCT-US99-17246-1

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5 930 100.0 930 16 US-09-124-233-1 Sequence 1, Appli
6 930 100.0 930 20 US-09-135-645-2 Sequence 2, Appli
7 930 100.0 930 37 US-09-884-814-2 Sequence 2, Appli
8 930 100.0 930 49 US-10-265-689-2 Sequence 2, Appli
9 930 100.0 960 1 PCT-US03-00253-131 Sequence 131, App
10 930 100.0 960 2 PCT-US03-00253-131 Sequence 131, App
11 930 100.0 960 50 US-10-336-472-131 Sequence 131, App
12 930 100.0 1105 18 US-09-277-575-7 Sequence 131, App
13 930 100.0 1105 25 US-09-599-760-3 Sequence 3, Appli
14 930 100.0 1105 31 US-09-711-022-7 Sequence 3, Appli
15 930 100.0 1105 34 US-09-823-886A-3 Sequence 7, Appli
16 930 100.0 1105 34 US-09-823-886A-3 Sequence 3, Appli
17 930 100.0 1131 1 PCT-US99-01198-4 Sequence 4, Appli
18 930 100.0 1131 2 PCT-US99-01198-4 Sequence 4, Appli
19 930 100.0 1131 15 US-09-012-218-4 Sequence 4, Appli
20 930 100.0 1185 40 US-09-949-016-3539 Sequence 3539, Ap
21 930 100.0 1612 20 US-09-353-645-13 Sequence 13, Appli
22 930 100.0 1612 49 US-10-265-689-13 Sequence 13, Appli
23 930 100.0 1617 47 US-10-170-235-27184 Sequence 27184, A
24 930 100.0 1643 48 US-10-240-965-183 Sequence 183, App
25 930 100.0 1643 73 US-10-195-106-183 Sequence 183, App
26 930 100.0 1646 47 US-10-159-563-344 Sequence 344, App
27 930 100.0 1646 53 PCT-US99-17246-5 Sequence 426, App
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40 928.4 99.8 940 15 US-09-012-218-5 Sequence 5, Appli
41 928.4 99.8 1596 13 US-08-807-861-38 Sequence 38, Appli
42 928.4 99.8 1596 14 US-08-946-719-38 Sequence 38, Appli
43 928.4 99.8 1882 1 PCT-US99-12623-3 Sequence 3, Appli
44 928.4 99.8 1882 2 PCT-US99-12623-3 Sequence 3, Appli
45 928.4 99.8 1882 15 US-09-093-662-3 Sequence 3, Appli

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ALIGNMENTS

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RESULT 1
PCT-US99-06317-2
; Sequence 2, Application PC/TUS9906317
; GENERAL INFORMATION:
; APPLICANT: Garvey, W. Timothy
; APPLICANT: Argyropoulos, George
; TITLE OF INVENTION: METHODS FOR IDENTIFYING A RISK TO UCP2 AND UCP3
; TITLE OF INVENTION: GENE VARIANT-RELATED AFFLICTIONS AND COMPOSITIONS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 19113.0069/P
; CURRENT APPLICATION NUMBER: PCT/US99/06317
; CURRENT FILING DATE: 1999-03-23
; EARLIER FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(930)
; OTHER INFORMATION: Note://corresponds to the mRNA for human UCP2
PCT-US99-06317-2
Query Match 100.0%; Score 930; DB 1; Length 930;

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Best Local Similarity 100.0%; Pred. No. 2.5e-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 ATGGTTGGGTTTCAGAGGCGACAGATGTGCCCCCTCACTGCACTGTAAGTTTCTTGGGGCT 60
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RESULT 2
PCT-US99-17246-1
; Sequence 1, Application PC/TUS9917246
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long

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/ APPLICANT: Amaral, M. Catherine
 / APPLICANT: Tularik Inc.
 / TITLE OF INVENTION: Uncoupling Protein 2 (hUCP2): Compositions and
 / TITLE OF INVENTION: Methods of Use
 / FILE REFERENCE: 018781-001100PC
 / CURRENT APPLICATION NUMBER: PCT/US99/17246
 / EARLIER FILING DATE: 1999-07-29
 / EARLIER APPLICATION NUMBER: US 09/124,293
 / NUMBER OF SEQ ID NOS: 8
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 1
 / LENGTH: 930
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)...(930)
 / OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
 PCT-US99-17246-1

Query Match 100.0%; Score 930; DB 1; Length 930;
 Best Local Similarity 100.0%; Pred. No. 2.5e-237;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 ATGTTGGGTTCAAGGCGACAGATGCCCCCTACGCGCACTGTGAAGTTCTTGAGGCT 60
 QY 61 GGACAGCTGCTGTCATCGAGATCTCATACCTTTCTTGATGTAAGTCTGTAAGTCCG 120
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 QY 121 TTACAGATCCAGAGAAAGTCAAGGGGCGAGTGGGCGCTCAAGCCAGCCGCAATGCCG 180
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 DB 901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930

RESULT 3

PCT-US99-06317-2
 / Sequence 2, Application PC/TUS9906317

/ GENERAL INFORMATION:
 / APPLICANT: Garvey, W. Timothy
 / APPLICANT: Artyopoulos, George
 / TITLE OF INVENTION: METHODS FOR IDENTIFYING A RISK TO UCP2 AND UCP3
 / TITLE OF INVENTION: GENE VARIANT-RELATED AFFILIATIONS AND COMPOSITIONS
 / TITLE OF INVENTION: THEREOF
 / FILE REFERENCE: 19113.0069/P
 / CURRENT APPLICATION NUMBER: PCT/US99/06317
 / EARLIER FILING DATE: 1999-03-23
 / EARLIER APPLICATION NUMBER: 60/078,972
 / EARLIER FILING DATE: 1998-03-23
 / NUMBER OF SEQ ID NOS: 41
 / SOFTWARE: FastSeq for Windows Version 3.0
 / SEQ ID NO: 2
 / LENGTH: 930
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)...(930)
 / OTHER INFORMATION: Note:/corresponds to the mRNA for human UCP2
 PCT-US99-06317-2

Query Match 100.0%; Score 930; DB 2; Length 930;
 Best Local Similarity 100.0%; Pred. No. 2.5e-237;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 ATGTTGGGTTCAAGGCGACAGATGCCCCCTACGCGCACTGTGAAGTTCTTGAGGCT 60
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 QY 121 TTACAGATCCAGAGAAAGTCAAGGGGCGAGTGGGCGCTCAAGCCAGCCGCAATGCCG 180
 DB 121 TTACAGATCCAGAGAAAGTCAAGGGGCGAGTGGGCGCTCAAGCCAGCCGCAATGCCG 180
 QY 181 GGTGTGATGGGCGACCATCTGACCATGATGATGATGATGATGATGATGATGATGATGAT 240
 DB 181 GGTGTGATGGGCGACCATCTGACCATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 241 GGGGTGTTGCGCGCTGCGAGCGCCAAATGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 GGGGTGTTGCGCGCTGCGAGCGCCAAATGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 301 GATTCGTCAAAAGTTCTACCAAGGGGCTGAGAGTCAAGCATTTGGAGAGCCGCTC 360
 DB 301 GATTCGTCAAAAGTTCTACCAAGGGGCTGAGAGTCAAGCATTTGGAGAGCCGCTC 360
 QY 361 CTAGCAGGCGACACCAAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420

QY 541 CCCAATGTTGCTGTAATGCCATTTGCAACTGCTGAGCTGTGACCTATGACCTATC 600
 Db 541 CCCAATGTTGCTGTAATGCCATTTGCAACTGCTGAGCTGTGACCTATGACCTATC 600
 QY 601 AAGATGCTCCTCTGAAAGCAACCTCATGACGATGACCTCCCTTGCCACTTCACTTCT 660
 Db 601 AAGATGCTCCTCTGAAAGCAACCTCATGACGATGACCTCCCTTGCCACTTCACTTCT 660
 QY 661 GCCTTTGGGCGAGGCTTCTGACCACTGTGATGCTCTCCCTGTGAGCTGTGCAAGC 720
 Db 661 GCCTTTGGGCGAGGCTTCTGACCACTGTGATGCTCTCCCTGTGAGCTGTGCAAGC 720
 QY 721 AGATACATGAACCTGCTGCTGGGCGAGTACAGAGGCTGGCCACTGTGCTTACCATG 780
 Db 721 AGATACATGAACCTGCTGCTGGGCGAGTACAGAGGCTGGCCACTGTGCTTACCATG 780
 QY 781 CTCGAGAAGAGGCGCCCGAGGCTTCTACAAAGGCTTCAATGCTCTTCTCCGCTTG 840
 Db 781 CTCGAGAAGAGGCGCCCGAGGCTTCTACAAAGGCTTCAATGCTCTTCTCCGCTTG 840
 QY 841 GGTTCCTGGAACGTGTGATGTCTGCACTATGACGAGTGAAGAGCTTCAATGCT 900
 Db 841 GGTTCCTGGAACGTGTGATGTCTGCACTATGACGAGTGAAGAGCTTCAATGCT 900
 QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 Db 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930

RESULT 7

US-09-884-814-2
 ; Sequence 2, Application US/09884814
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Amaral, M. Catherine
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
 ; TITLE OF INVENTION: Methods of Use
 ; FILE REFERENCE: 018781-00110US
 ; CURRENT APPLICATION NUMBER: US/09/884,814
 ; CURRENT FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: US 09/124,293
 ; PRIOR FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(930)
 ; OTHER INFORMATION: human uncoupling Protein 2 (hUCP2) Chen (Tularik)
 ; US-09-884-814-2

Query Match 100.0%; Score 930; DB 37; Length 930;
 Best Local Similarity 100.0%; Pred. No. 2.5e-237;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGGGTTTCAAGGCCACAGATGTGCCCCCTTACTGCACTGTGAAGTTTCTTGGGGCT 60
 Db 1 ATGTTGGGTTTCAAGGCCACAGATGTGCCCCCTTACTGCACTGTGAAGTTTCTTGGGGCT 60
 QY 61 GGCACAGCTGCTGATGACGATCTCATCACTTCTCTGATGATGCTTAAAGTCCG 120
 Db 61 GGCACAGCTGCTGATGACGATCTCATCACTTCTCTGATGATGCTTAAAGTCCG 120
 QY 121 TTACAGATCCAAAGAGAAAGTCAAGGCGCAAGTGGCGTACAGCCAGCCGCTACCCG 180
 Db 121 TTACAGATCCAAAGAGAAAGTCAAGGCGCAAGTGGCGTACAGCCAGCCGCTACCCG 180
 QY 181 GGTGTGATGGGACCATTTCTGACCATGTGTGTAAGAGGCCCCCGAAGCCTTCAAT 240

Db 181 GGTGTGATGGGACCATTTCTGACCATGTGTGTAAGAGGCCCCCGAAGCCTTCAAT 240
 QY 241 GGGCTGTGTGCGGCTCTGAGCGCCAAATAGCTTTGCTGTGCGCATGCGCTGAT 300
 Db 241 GGGCTGTGTGCGGCTCTGAGCGCCAAATAGCTTTGCTGTGCGCATGCGCTGAT 300
 QY 301 GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGATGACACATTTGGAGCGCTC 360
 Db 301 GATTCTGTCAACAGTTCTTACACCAAGGCTCTGAGATGACACATTTGGAGCGCTC 360
 QY 361 CTAGCAGGACGACACACAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420
 Db 361 CTAGCAGGACGACACACAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420
 QY 421 AAGTCCGATTCGAAGCTCAAGGCGCGGCTGAGAGGTGTGTGAGATACCAAGCACCGTC 480
 Db 421 AAGTCCGATTCGAAGCTCAAGGCGCGGCTGAGAGGTGTGTGAGATACCAAGCACCGTC 480
 QY 481 AATGCTTACAAACCATTTGCTGAGAGAGAGGTTCCGAGGCTTGTGAAAGGACCTCT 540
 Db 481 AATGCTTACAAACCATTTGCTGAGAGAGAGGTTCCGAGGCTTGTGAAAGGACCTCT 540
 QY 541 CCCAATGTTGCTGTAATGCCATTTGCAACTGCTGAGCTGTGACCTATGACCTATC 600
 Db 541 CCCAATGTTGCTGTAATGCCATTTGCAACTGCTGAGCTGTGACCTATGACCTATC 600
 QY 601 AAGATGCTCCTCTGAAAGCAACCTCATGACGATGACCTCCCTTGCCACTTCACTTCT 660
 Db 601 AAGATGCTCCTCTGAAAGCAACCTCATGACGATGACCTCCCTTGCCACTTCACTTCT 660
 QY 661 GCCTTTGGGCGAGGCTTCTGACCACTGTGATGCTCTCCCTGTGAGCTGTGCAAGC 720
 Db 661 GCCTTTGGGCGAGGCTTCTGACCACTGTGATGCTCTCCCTGTGAGCTGTGCAAGC 720
 QY 721 AGATACATGAACCTGCTGCTGGGCGAGTACAGAGGCTGGCCACTGTGCTTACCATG 780
 Db 721 AGATACATGAACCTGCTGCTGGGCGAGTACAGAGGCTGGCCACTGTGCTTACCATG 780
 QY 781 CTCGAGAAGAGGCGCCCGAGGCTTCTACAAAGGCTTCAATGCTCTTCTCCGCTTG 840
 Db 781 CTCGAGAAGAGGCGCCCGAGGCTTCTACAAAGGCTTCAATGCTCTTCTCCGCTTG 840
 QY 841 GGTTCCTGGAACGTGTGATGTCTGCACTATGACGAGTGAAGAGCTTCAATGCT 900
 Db 841 GGTTCCTGGAACGTGTGATGTCTGCACTATGACGAGTGAAGAGCTTCAATGCT 900
 QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930
 Db 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930

RESULT 8

US-10-265-669-2
 ; Sequence 2, Application US/10265669
 ; GENERAL INFORMATION:
 ; APPLICANT: SURWIT, RICHARD S.
 ; APPLICANT: COLLINS, SHEILA A.
 ; APPLICANT: WARDEN, CRAIG H.
 ; APPLICANT: SELDIN, MICHAEL P.
 ; APPLICANT: RICOUEUR, DANIEL
 ; APPLICANT: BOUILLAUD, FREDERIC
 ; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
 ; FILE REFERENCE: 1579-376
 ; CURRENT APPLICATION NUMBER: US/10/265,669
 ; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/353,645
 ; PRIOR FILING DATE: 1999-07-15
 ; PRIOR APPLICATION NUMBER: PCT/US97/06864
 ; PRIOR FILING DATE: 1997-04-22
 ; PRIOR APPLICATION NUMBER: 60/034,960
 ; PRIOR FILING DATE: 1997-01-15
 ; NUMBER OF SEQ ID NOS: 47

361 CTAGCAGGCAGCACCAAGTGCCCTGGCTGTGGCTGTGGCCAGCCACCGATGTGTA 420


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Db      375 CTAGCAGGAGGAGCCAGAGTCCCTGGCTGTGTGTGGCCAGACCCAGAGTGTGTA 434
Qy      421 AAGTCCGATTCAGAGCTAGGCGCGGCTGAGAGTGTGCGAGATACCAAGACCGTC 480
Db      435 AAGTCCGATTCAGAGCTAGGCGCGGCTGAGAGTGTGCGAGATACCAAGACCGTC 494
Qy      481 AATGCTTACAGACATTCGCGAGAGAGAGGATTCGAGGCTCTGAGAAAGACCTCT 540
Db      495 AATGCTTACAGACATTCGCGAGAGAGAGGATTCGAGGCTCTGAGAAAGACCTCT 554
Qy      541 CCCAATGTGCTGTATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db      555 CCCAATGTGCTGTATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
Qy      601 AAGATGCTCCCTGGAAGCAACCTCATAGACATGACCTCCCTGCACTTCACTTCT 660
Db      615 AAGATGCTCCCTGGAAGCAACCTCATAGACATGACCTCCCTGCACTTCACTTCT 674
Qy      661 GCCTTTGGGCGAGGCTTGTGCACTGTCATGCTCCCTGTGAGCTGTGTCAAGC 720
Db      675 GCCTTTGGGCGAGGCTTGTGCACTGTCATGCTCCCTGTGAGCTGTGTCAAGC 734
Qy      721 AGATACATGAACCTGCTGCTGCGACATGAGAGGCTGCGCACTGCTTACCATG 780
Db      735 AGATACATGAACCTGCTGCTGCGACATGAGAGGCTGCGCACTGCTTACCATG 794
Qy      781 CTCAGAGAGAGGAGGCGCGAGGCTTCTACAAAGGTTATGCTCTTCTCGGCTTG 840
Db      795 CTCAGAGAGAGGAGGCGCGAGGCTTCTACAAAGGTTATGCTCTTCTCGGCTTG 854
Qy      841 GGTTCCTGGAACGATGATGTCATGCTATGAGACATGAGAGGCTGCTGCTGCTGCT 900
Db      855 GGTTCCTGGAACGATGATGTCATGCTATGAGACATGAGAGGCTGCTGCTGCTGCT 914
Qy      901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930
Db      915 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 944

```

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RESULT 10
PCT-US03-00253-131
; Sequence 131, Application PC/TUS0300253
; GENERAL INFORMATION:
; APPLICANT: Curagen Corp. et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-533C-061 (CURA 833C WO)
; CURRENT APPLICATION NUMBER: PCT/US03/00253
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/092,900
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 10/136,826
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 10/236,417
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/345,092
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/345,219
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/348,804
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/349,182
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/349,733
; PRIOR FILING DATE: 2002-01-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 131

```

```

; LENGTH: 960
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(941)
PCT-US03-00253-131

Query Match      100.0%; Score 930; DB 2; Length 960;
Best Local Similarity 100.0%; Pred. No. 2,6e-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AATGTTGGATTCAGAGCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db      15 AATGTTGGATTCAGAGCCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 74
Qy      61 GGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db      75 GGCACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 134
Qy      121 TTACAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db      135 TTACAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
Qy      181 GGTGTGATGAGGACCATCTGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db      195 GGTGTGATGAGGACCATCTGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 254
Qy      241 GGGCTGTGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db      255 GGGCTGTGTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
Qy      301 GATTCGTCAACAGTTCCTACACCAAGGCTCTGAGCATGCGACATTTGGAGGCGGCTC 360
Db      315 GATTCGTCAACAGTTCCTACACCAAGGCTCTGAGCATGCGACATTTGGAGGCGGCTC 374
Qy      361 CTAGCAGGAGCAGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db      375 CTAGCAGGAGCAGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 434
Qy      421 AAGTCCGATTCAGAGCTAGGCGCGGCTGAGAGTGTGCGAGATACCAAGACCGTC 480
Db      435 AAGTCCGATTCAGAGCTAGGCGCGGCTGAGAGTGTGCGAGATACCAAGACCGTC 494
Qy      481 AATGCTTACAGACATTCGCGAGAGAGAGGATTCGAGGCTCTGAGAAAGACCTCT 540
Db      495 AATGCTTACAGACATTCGCGAGAGAGAGGATTCGAGGCTCTGAGAAAGACCTCT 554
Qy      541 CCCAATGTGCTGTATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db      555 CCCAATGTGCTGTATGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
Qy      601 AAGATGCTCCCTGGAAGCAACCTCATAGACATGACCTCCCTGCACTTCACTTCT 660
Db      615 AAGATGCTCCCTGGAAGCAACCTCATAGACATGACCTCCCTGCACTTCACTTCT 674
Qy      661 GCCTTTGGGCGAGGCTTGTGCACTGTCATGCTCCCTGTGAGCTGTGTCAAGC 720
Db      675 GCCTTTGGGCGAGGCTTGTGCACTGTCATGCTCCCTGTGAGCTGTGTCAAGC 734
Qy      721 AGATACATGAACCTGCTGCTGCGACATGAGAGGCTGCGCACTGCTTACCATG 780
Db      735 AGATACATGAACCTGCTGCTGCGACATGAGAGGCTGCGCACTGCTTACCATG 794
Qy      781 CTCAGAGAGAGGAGGCGCGAGGCTTCTACAAAGGTTATGCTCTTCTCGGCTTG 840
Db      795 CTCAGAGAGAGGAGGCGCGAGGCTTCTACAAAGGTTATGCTCTTCTCGGCTTG 854
Qy      841 GGTTCCTGGAACGATGATGTCATGCTATGAGACATGAGAGGCTGCTGCTGCTGCTGCT 900
Db      855 GGTTCCTGGAACGATGATGTCATGCTATGAGACATGAGAGGCTGCTGCTGCTGCTGCT 914
Qy      901 GCCTGCACTTCCGAGAGGCTCCCTTCTGA 930

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Db 915 GCCTGCACTTCCCGAGAGGCTCCCTCTGTA 944

RESULT 11 US-10-336-472-131

Sequence 131, Application US/10336472

GENERAL INFORMATION:

APPLICANT: Anderson, David W.
APPLICANT: Ballinger, Robert A.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Chant, John S.
APPLICANT: Berghs, Constance
APPLICANT: Gangoli, Esna A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Furtak, Katarzyna
APPLICANT: Gerlach, Valerie
APPLICANT: Gilbert, Jennifer A.
APPLICANT: Gunther, Erik
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia Sasha
APPLICANT: Li, J.
APPLICANT: Liu, Xiaohong
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Isabelle
APPLICANT: Padigaru, Muralidhara
APPLICANT: Paturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: MacDougall, John R.
APPLICANT: Mishra, Vishnu
APPLICANT: Pera, Carol E.A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Shukets, Richard A.
APPLICANT: Smithson, Glenda
APPLICANT: Spytek, Kimberly A.
APPLICANT: Stone, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Ore, Tatiana
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Tchiernev, Velizar T.
APPLICANT: Verneil, Corine A.M.
APPLICANT: Wolenc, Adam R.
APPLICANT: Zerhusen, Bryan D.

TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-535C

CURRENT APPLICATION NUMBER: US/10/336,472

PRIOR FILING DATE: 2003-01-03

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2001-12-04

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-10-26

PRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2002-05-01

PRIOR FILING DATE: 2002-09-06

PRIOR FILING DATE: 2002-01-04

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 230
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 131
LENGTH: 960
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (15) .. (941)
US-10-336-472-131

Query Match 100.0%; Score 930; DB 50; Length 960;
Best Local Similarity 100.0%; Pred. No. 2,66-237;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGTTGGGTTCAAGGCCACAGATGTCCTTCTGCTGCACTGTGAAGTTCTTGGGCT 60
15 ATGGTTGGGTTCAAGGCCACAGATGTCCTTCTGCTGCACTGTGAAGTTCTTGGGCT 74
61 GGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
75 GGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 134
121 TTACAGATCCAG 180
135 TTACAGATCCAG 194
181 GGTTGATGGGACCACTTCTGACCATGATGGGCTGATGAGAGAGAGAGAGAGAGAGAG 240
195 GGTTGATGGGACCACTTCTGACCATGATGGGCTGATGAGAGAGAGAGAGAGAGAGAG 254
241 GGCTGATGGGACCACTTCTGACCATGATGGGCTGATGAGAGAGAGAGAGAGAGAGAG 300
255 GGCTGATGGGACCACTTCTGACCATGATGGGCTGATGAGAGAGAGAGAGAGAGAGAG 314
301 GATTCGTCAAG 360
315 GATTCGTCAAG 374
361 CTAGCAG 420
375 CTAGCAG 434
421 AAGTCCGATTCAG 480
435 AAGTCCGATTCAG 494
481 AATGCCCTACAG 540
495 AATGCCCTACAG 554
541 CCAGATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
555 CCAGATGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 614
601 AAG 660
615 AAG 674
661 GGCTTTGGGAG 720
675 GGCTTTGGGAG 734
721 AGATACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 780
735 AGATACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 794
781 CTCAG 840
795 CTCAG 854
841 GGTTCCGAG 900

Db 855 GGTTCCTGGAACGTGTATGTTCTGACCTATGACGACTGAACGAGCCCTCATGGCT 914

QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTTCTGA 930

Db 915 GCCTGCACTTCCCGAGAGGCTCCCTTTCTGA 944

RESULT 12

US-09-277-575-7

; Sequence 7, Application US/09277575

; GENERAL INFORMATION:

; APPLICANT: Newell, Martha K.

; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO

; FILE REFERENCE: WO139/7028/HK

; CURRENT APPLICATION NUMBER: US/09/277,575

; EARLIER FILING DATE: 1999-03-26

; EARLIER APPLICATION NUMBER: U.S. 60/082,250

; EARLIER FILING DATE: 1998-04-17

; EARLIER APPLICATION NUMBER: U.S. 60/094,519

; EARLIER FILING DATE: 1998-07-29

; EARLIER APPLICATION NUMBER: U.S. 60/101,580

; EARLIER FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 1105

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-09-277-575-7

Query Match 100.0%; Score 930; DB 18; Length 1105;

Best Local Similarity 100.0%; Pred. No. 2.7e-237;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGGTTCAAGGCAAGATGTCGCGGCTGACCTGACCTGTAAGTTCTTGGGCT 60

Db 89 ATGGTGGGTTCAAGGCAAGATGTCGCGGCTGACCTGACCTGTAAGTTCTTGGGCT 148

QY 61 GGCACAGCTGCTGCAATCGCAATCTCATACCTTCTCTGTAATCTGTAATCTGCGG 120

Db 149 GGCACAGCTGCTGCAATCGCAATCTCATACCTTCTCTGTAATCTGTAATCTGCGG 208

QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTACAGCCAGCCGACAGTACCC 180

Db 209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTACAGCCAGCCGACAGTACCC 268

QY 181 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 240

Db 269 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 328

QY 241 GGGCTGTGCTGGGCTGCAAGGCAATGAGTTGGCTGCTGCTGCGGCTGAT 300

Db 329 GGGCTGTGCTGGGCTGCAAGGCAATGAGTTGGCTGCTGCTGCGGCTGAT 388

QY 301 GATCTGTCAAAAGAGTTCTACACCAAGGCTCTGACATGCGCAATGGAGCCGCTC 360

Db 389 GATCTGTCAAAAGAGTTCTACACCAAGGCTCTGACATGCGCAATGGAGCCGCTC 448

QY 361 CTAGCAGCAGCAACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 449 CTAGCAGCAGCAACCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508

QY 421 AAGTCCGATTCAGAGCTCAGGCGCGGCTGAGGTGTGAGATACCAAGCAACGCTC 480

Db 509 AAGTCCGATTCAGAGCTCAGGCGCGGCTGAGGTGTGAGATACCAAGCAACGCTC 568

QY 491 AATGCTTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGGCTCTGGAAGAGGACTCT 540

Db 569 AATGCTTCAAGACCATTTGCCGAGAGAGAGGTTCCGGGGCTCTGGAAGAGGACTCT 628

QY 541 CCAATGTGCTCGAATGAGCTATGCTCACTGTGCTGCTGCTGCTGCTGCTGCTGCT 600

Db 629 CCAATGTGCTCGAATGAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688

QY 601 AAGATGCGCTTCCGAAAGCAACCTCATGACATGACATGACATGACATGACATGAC 660

Db 669 AAGATGCGCTTCCGAAAGCAACCTCATGACATGACATGACATGACATGACATGAC 748

QY 661 GCCTTGGGGGAGGCTTCTGCAACCATGTCATGCTCCCTGTGACAGTGTCAAGAG 720

Db 749 GCCTTGGGGGAGGCTTCTGCAACCATGTCATGCTCCCTGTGACAGTGTCAAGAG 808

QY 721 AATATCATGACTTCCCTGCGGCAATGACATGACATGACATGACATGACATGACAT 780

Db 809 AATATCATGACTTCCCTGCGGCAATGACATGACATGACATGACATGACATGACAT 868

QY 781 CTCAGAAAGAGGAGGCGCGGCACTTCAAGAGGTTCAAGGCTTCTGCTGCTGCTG 840

Db 869 CTCAGAAAGAGGAGGCGCGGCACTTCAAGAGGTTCAAGGCTTCTGCTGCTGCTG 928

QY 841 GGTTCCTGGAACGTGTGATGTTGTCACCTATGAGAGAGTGAAGAGGCTCATGGCT 900

Db 929 GGTTCCTGGAACGTGTGATGTTGTCACCTATGAGAGAGTGAAGAGGCTCATGGCT 988

QY 901 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 930

Db 989 GCCTGCACTTCCCGAGAGGCTCCCTTCTGA 1018

RESULT 13

US-09-599-760-3

; Sequence 3, Application US/09599760

; GENERAL INFORMATION:

; APPLICANT: Newell, Martha K.

; TITLE OF INVENTION: Methods and Products for Manipulating

; FILE REFERENCE: 10277/7009

; CURRENT APPLICATION NUMBER: US/09/599,760

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: US 60/140,574

; PRIOR FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3

; LENGTH: 1105

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-599-760-3

Query Match 100.0%; Score 930; DB 25; Length 1105;

Best Local Similarity 100.0%; Pred. No. 2.7e-237;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGGTTCAAGGCAAGATGTCGCGGCTGACCTGACCTGTAAGTTCTTGGGCT 60

Db 89 ATGGTGGGTTCAAGGCAAGATGTCGCGGCTGACCTGACCTGTAAGTTCTTGGGCT 148

QY 61 GGCACAGCTGCTGCAATCGCAATCTCATACCTTCTCTGTAATCTGTAATCTGCGG 120

Db 149 GGCACAGCTGCTGCAATCGCAATCTCATACCTTCTCTGTAATCTGTAATCTGCGG 208

QY 121 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTACAGCCAGCCGACAGTACCC 180

Db 209 TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGGCTACAGCCAGCCGACAGTACCC 268

QY 181 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 240

Db 269 GGTGTGATGGGCAACATTTGACCATGTGTGCTGAGAGGCCCCGAAAGCTTCAAT 328

QY 241 GGGCTGTGCTGGGCTGCAAGGCAATGAGTTGGCTGCTGCTGCTGCTGCTGCTGCT 300

Db 329 GGGCTGTGCTGGGCTGCAAGGCAATGAGTTGGCTGCTGCTGCTGCTGCTGCTGCT 388

QY 301 GATCTGTCAAAAGAGTTCTACACCAAGGCTCTGAGCATGCGATTTGGAGCGGCTC 360

; PRIOR FILING DATE: 1998-07-23
 ; PRIOR APPLICATION NUMBER: US 60/101,580
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 7
 ; LENGTH: 1105
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-711-022A-7

Query Match 100.0%; Score 930; DB 31; Length 1105;
 Best Local Similarity 100.0%; Pred. No. 2,76-237;
 Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGTTGGGTTCAAGCCACAGATGCCCCCTACTGACCACTGAAAGTTTCTTGGGGCT	60
DB	89	ATGTTGGGTTCAAGCCACAGATGCCCCCTACTGACCACTGAAAGTTTCTTGGGGCT	148
QY	61	GGCAGAGTGTGCTGATCGAGATCTCATACCTTTCCTGATATCTGCTAAAGTCGG	120
DB	149	GGCAGAGTGTGCTGATCGAGATCTCATACCTTTCCTGATATCTGCTAAAGTCGG	208
QY	121	TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGGCTACAGCCAGCCAGTACCG	180
DB	209	TTACAGATCCAGAGAAAGTCAAGGGCCAGTGGCGGCTACAGCCAGCCAGTACCG	268
QY	181	GGTGTATGGGACCAATTCGACCATGTGCTACTGAGGGCCCCGGAAGCCTCTACAT	240
DB	269	GGTGTATGGGACCAATTCGACCATGTGCTACTGAGGGCCCCGGAAGCCTCTACAT	328
QY	241	GGGCTGTGTCGGGCTGACGGCCCAATGAGCTTTGCTTCTGCTGCGCATGGCCTGAT	300
DB	329	GGGCTGTGTCGGGCTGACGGCCCAATGAGCTTTGCTTCTGCTGCGCATGGCCTGAT	388
QY	301	GATCTGTCAAAAGTTCTACACCAAGGGCTGAGCATGCGAGATTGGAGCCGCTC	360
DB	389	GATCTGTCAAAAGTTCTACACCAAGGGCTGAGCATGCGAGATTGGAGCCGCTC	448
QY	361	CTAGCAGGACGACCAAGGTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTG	420
DB	449	CTAGCAGGACGACCAAGGTGCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTG	508
QY	421	AAGGTCCGATTCCAGCTCAGGCGCGGGCTGAGGTGTGAGATACCAAGCACCGTC	480
DB	509	AAGGTCCGATTCCAGCTCAGGCGCGGGCTGAGGTGTGAGATACCAAGCACCGTC	568
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DB	569	AATGCTCAAGACCAATGCGCGAGAGAAAGGTTCCGGGGCTCTGAAAGGACCTCT	628
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DB	629	CCCAATGTGCTGCTAATGCACTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	688
QY	601	AAGATGCTCTCTGAAGCCCACTCATGACAGATGACCTCCCTTGGCACTTCTCT	660
DB	689	AAGATGCTCTCTGAAGCCCACTCATGACAGATGACCTCCCTTGGCACTTCTCT	748
QY	661	GCTTTGGGGGAGGCTTCTGACCACTGATGAGCTCCCTGCTGAGCGTGGTCAAGAG	720
DB	749	GCTTTGGGGGAGGCTTCTGACCACTGATGAGCTCCCTGCTGAGCGTGGTCAAGAG	808
QY	721	AGATACATGAATCTGCTGAGCTGAGCAAGTACAGCTGCGCACTGTGCCCTTACATG	780
DB	809	AGATACATGAATCTGCTGAGCTGAGCAAGTACAGCTGCGCACTGTGCCCTTACATG	868
QY	781	CTCAGAGAGAGGGGCTTCTGACCACTGATGAGCTCCCTGCTGAGCGTGGTCAAGAG	840
DB	869	CTCAGAGAGAGGGGCTTCTGACCACTGATGAGCTCCCTGCTGAGCGTGGTCAAGAG	928
QY	841	GGTTCCTGAAAGTGTGATGTGTGCACTATGAGCAGCTGAAAGAGCCCTCATGGCT	900

DB	929	GGTTCCTGAAAGTGTGATGTGTGCACTATGAGCAGCTGAAAGAGCCCTCATGGCT	988
QY	901	GCTGCACTTCCGAGAGGCTCCCTTCTGA	930
DB	989	GCTGCACTTCCGAGAGGCTCCCTTCTGA	1018

Search completed: February 4, 2004, 21:15:07
 Job time : 3501 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 18:21:03 ; Search time 413 Seconds
(without alignments)
6494.407 Million cell updates/sec

Title: US-09-884-814-2

Perfect score: 930
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4908811 seqs, 1442037763 residues

Total number of hits satisfying chosen parameters: 9817622

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	100.0	1105	US-09-599-760B-3	Sequence 3, Appl1
2	930	100.0	1105	US-10-616-865-7	Sequence 7, Appl1
3	927.6	99.7	1617	US-60-485-450-562	Sequence 562, App
4	820.4	88.2	930	US-60-507-481-2199	Sequence 1619, Ap
5	762	81.9	1575	US-10-743-643-169	Sequence 169, App
6	762	81.9	1575	US-60-493-007-1024	Sequence 1024, Ap
7	762	81.9	1575	US-60-531-341-500	Sequence 500, App
8	492.2	52.9	936	US-60-507-481-2196	Sequence 2196, Ap
9	472.4	50.8	2263	US-60-490-890-851	Sequence 851, App
10	421.4	45.3	674	PCT-US03-10141-263	Sequence 263, App
11	421.4	45.3	674	PCT-US03-14632-406	Sequence 406, App
12	421.4	45.3	674	US-10-404-460-263	Sequence 263, App
13	411	44.2	1132	US-09-599-760B-5	Sequence 5, Appl1
14	411	44.2	1132	US-10-616-865-9	Sequence 9, Appl1
15	411	44.2	1182	US-10-743-643-171	Sequence 171, App
16	411	44.2	1182	US-60-490-890-853	Sequence 853, App
17	411	44.2	1182	US-60-531-341-502	Sequence 502, App
18	323	34.7	930	US-60-507-481-1614	Sequence 1614, App
19	309	33.2	573	US-10-332-859-107	Sequence 107, App
20	297	31.9	924	US-09-599-760B-1	Sequence 1, Appl1
21	297	31.9	924	US-10-616-865-5	Sequence 5, Appl1
22	234.6	25.2	406	US-10-745-457-2799	Sequence 2799, A
23	216	23.2	20145	US-60-485-450-12126	Sequence 12126, A
24	200.6	21.6	201	US-60-485-450-7844	Sequence 7844, Ap
25	200.6	21.6	201	US-60-485-450-7845	Sequence 7845, Ap

26	200.6	21.6	201	US-60-485-450-7850	Sequence 7850, Ap
27	200.6	21.6	201	US-60-485-450-7852	Sequence 7852, Ap
28	200.2	21.5	201	US-60-485-450-7848	Sequence 7848, Ap
29	182.4	19.6	1331	US-10-425-114A-77120	Sequence 27120, A
30	172.2	18.5	201	US-60-485-450-32420	Sequence 32420, A
31	167.6	18.0	201	US-60-485-450-32418	Sequence 32418, A
32	154.4	16.6	1535	US-10-671-628-1	Sequence 1, Appl1
33	144	15.5	201	US-60-485-450-32419	Sequence 32419, A
34	142	15.3	201	US-60-485-450-32424	Sequence 32424, A
35	138	14.8	366	US-10-755-149-1044	Sequence 1044, Ap
36	126.8	13.6	1023	US-09-614-150A-14018	Sequence 14018, A
37	107	11.5	761	US-10-425-114A-19049	Sequence 19049, A
38	106.4	11.4	201	US-60-485-450-32410	Sequence 32410, A
39	100.6	10.8	1561	US-60-531-341-1433	Sequence 1433, Ap
40	100.6	10.8	1570	US-10-743-643-1603	Sequence 1603, Ap
41	97	10.4	747	US-10-425-114A-4247	Sequence 4247, Ap
42	96	10.3	2931	US-10-671-628-3	Sequence 3, Appl1
43	91.6	9.8	1898	US-10-425-114A-6241	Sequence 6241, Ap
44	91	9.8	1654	US-09-614-150A-815	Sequence 815, Ap
45	91	9.8	3725	US-09-614-150A-814	Sequence 814, App

ALIGNMENTS

RESULT 1
US-09-599-760B-3
Sequence 3, Application US/09599760B
GENERAL INFORMATION:

APPLICANT: Newell, Martha R
TITLE OF INVENTION: Methods and products for manipulating uncoupling protein
FILE REFERENCE: V00139.76059.7603
CURRENT APPLICATION NUMBER: US/09/599,760B
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/140,574
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent version 3.2
SEQ ID NO 3
LENGTH: 1105
TYPE: DNA
ORGANISM: Homo sapiens
US-09-599-760B-3

Query Match	100.0%;	Score 930;	DB 5;	Length 1105;
Best Local Similarity	100.0%;	Pred. No. 1.4e-257;	Indels 0;	Gaps 0;
Matches 930;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCTTGTTCAAGCCACAGATGTCCTTCACTGCACTGTGAAGTTCTTGCGACT	60	
DB	89	ATGCTTGTTCAAGCCACAGATGTCCTTCACTGCACTGTGAAGTTCTTGCGACT	148	
QY	61	GGCAGCTGCTTCGATCGCATCTTCATCAGTTTCTTCTTGATATCTTAAGTCGGG	120	
DB	149	GGCAGCTGCTTCGATCGCATCTTCATCAGTTTCTTCTTGATATCTTAAGTCGGG	208	
QY	121	TTACAGATCCAGAGAAATGTCAGGGCCAGTGCCTGACAGCCAGCCAGTACGCG	180	
DB	209	TTACAGATCCAGAGAAATGTCAGGGCCAGTGCCTGACAGCCAGCCAGTACGCG	268	
QY	181	GGTGTGATGGGCAACATTCATGACATGTGCTGTAAGAGGCCCCGAAAGCTTACAT	240	
DB	269	GGTGTGATGGGCAACATTCATGACATGTGCTGTAAGAGGCCCCGAAAGCTTACAT	328	
QY	241	GGGCTGTGTCGGGCTTCGAGGCGCAATGAGTTTGCTGTCCGATCGGCTGAT	300	
DB	329	GGGCTGTGTCGGGCTTCGAGGCGCAATGAGTTTGCTGTCCGATCGGCTGAT	388	
QY	301	GATTCTGCAACAGTTCTACACCAAGGCTCTGACATGCAAGATTGGAGCGGCTTC	360	
DB	389	GATTCTGCAACAGTTCTACACCAAGGCTCTGACATGCAAGATTGGAGCGGCTTC	448	

Qy	361	CTAGCAGGACAGACCAACAGTATCCCTGGCTGTGGTGTGGCCAGGCCCAAGATATGTGTGA	420
Dd	449	CTAGCAGGACAGACCAACAGTATCCCTGGCTGTGGTGTGGCCAGGCCCAAGATATGTGTGA	508
Qy	421	AAGSTCCGATTTCCAACTCTAGGCCCCGGGCTGGAGTGGTCCGGAATATCCAAACACCCATC	480
Dd	509	AAGSTCCGATTTCCAACTCTAGGCCCCGGGCTGGAGTGGTCCGGAATATCCAAAGACCGATC	568
Qy	481	AATGCCCTACAAGACCAATTCGCCGAGAGAGGGATTCGCGGACCTCTTGAAAAGGACCTCT	540
Dd	569	AATGCCCTACAAGACCAATTCGCCGAGAGAGGGATTCGCGGACCTCTTGAAAAGGACCTCT	628
Qy	541	CCCAATGTTGCTGTGAATAGCCATGTGCATCTGTGTAGCTGTGGAGACTTATGAACCTATC	600
Dd	629	CCCAATGTTGCTGTGAATAGCCATGTGCATCTGTGTAGCTGTGGAGACTTATGAACCTATC	688
Qy	601	AAGAGTACCCTCCTGANAAGCCAACTCATGACAGATGAACCTCCCTTGCCACTTCACTTCT	660
Dd	689	AAGAGTACCCTCCTGANAAGCCAACTCATGACAGATGAACCTCCCTTGCCACTTCACTTCT	748
Qy	661	GCCTTTGGGGCAGGCTTCTTGACACACTGTGCATCGGCTCCCTGTAGACGTGTCAACACG	720
Dd	749	GCCTTTGGGGCAGGCTTCTTGACACACTGTGCATCGCTCCCTGTAGACGTGTCAACACG	808
Qy	721	AGATACATGAATCTTCGCTGGGACAGTACAGTACGCTGGCCACTGTGCCCTTACCATG	780
Dd	809	AGATACATGAATCTTCGCTGGGACAGTACAGTACGCTGGCCACTGTGCCCTTACCATG	868
Qy	781	CTCCAGAAAGAGGGGCCCCGAGCCTTCTCAAAAGGGTTCATAGCCCTCCTTCTCCGGTTG	840
Dd	869	CTCCAGAAAGAGGGGCCCCGAGCCTTCTCAAAAGGGTTCATAGCCCTCCTTCTCCGGTTG	928
Qy	841	GATTCCTGAAACGTGTGATATGTTGTCACCTTATGACAGCTGAACAGACCCCTCATGGCT	900
Dd	929	GATTCCTGAAACGTGTGATATGTTGTCACCTTATGACAGCTGAACAGACCCCTCATGGCT	988
Qy	901	GCTCGCACTTCCCGAAGGCTCCCTTCTTGA	930
Dd	989	GCTCGCACTTCCCGAAGGCTCCCTTCTTGA	1018

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RESULT 2
US-10-616-865-7
Sequence 7, Application US/10616865
GENERAL INFORMATION:
APPLICANT: NEWELL, MANTHA K
TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASES
FILE REFERENCE: V01.39, 700170600
CURRENT APPLICATION NUMBER: US/10/616, 865
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 09/277, 575
PRIOR FILING DATE: 1999-03-27
PRIOR APPLICATION NUMBER: US 60/082, 250
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/101, 580
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 60/094, 519
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 1105
TYPE: DNA
ORGANISM: Homo sapiens
US-10-616-865-7

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Query Match      100.0%   Score 930; DB 6; Length 1105;
Best Local Similarity 100.0%   Pred. No. 1,4e-257;
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB 89 ATGGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCGCATGTGAAGTTCTTGGGGCT 148

Qy	61	GGACAGCGCCGATCGAGATCTATCAACCTTCTCTGGATCTGTAAATCCG	120
Db	149	GGCAAGCTGCTGATTCGAGATCTATCACTTCTCTGGATCTGTAAATCCG	208
Qy	121	TTACAGATCOAAGAAAGTCAAGGGCCAGTGCCTCAAGCAGCCCCAGTCCG	180
Db	209	TTACAGATCOAAGAAAGTCAAGGGCCAGTGCCTCAAGCAGCCCCAGTCCG	268
Qy	181	GGGTATGGGACCAATCTGACCATGGTGGTACTAGAGGCCCGAAGCCTCTCAAT	240
Db	269	GGGTATGGGACCAATCTGACCATGGTGGTACTAGAGGCCCGAAGCCTCTCAAT	328
Qy	241	GGGCTGGTTCGGGCTTCAGCGCCAAATAGCTTTGCTCTGTCCGATTCGGCTGTAT	300
Db	329	GGGCTGGTTCGGGCTTCAGCGCCAAATAGCTTTGCTCTGTCCGATTCGGCTGTAT	388
Qy	301	GATTCGTCAACAGTTCTTACACCAAGGAGCTCTAGATCCAGCATTTGGAGCCGCTC	360
Db	389	GATTCGTCAACAGTTCTTACACCAAGGAGCTCTAGATCCAGCATTTGGAGCCGCTC	448
Qy	361	CTAGCAGGAGACCAACAAGTCCCTGGCTGTGGCTGTGGCCACAGCCAGATATGGTA	420
Db	449	CTAGCAGGAGACCAACAAGTCCCTGGCTGTGGCTGTGGCCACAGCCAGATATGGTA	508
Qy	421	AAGTCCGATTCGAAGCTCAGGCCCGGAGCTGAGGTGATCGAGATACCAAGACCTGT	480
Db	509	AAGTCCGATTCGAAGCTCAGGCCCGGAGCTGAGGTGATCGAGATACCAAGACCTGT	568
Qy	481	AATGCTTAACAACCAATTCGCCGAGAGGAGAGGTTCCGGGGCCTCTGAAAGGAGCCTT	540
Db	569	AATGCTTAACAACCAATTCGCCGAGAGGAGAGGTTCCGGGGCCTCTGAAAGGAGCCTT	628
Qy	541	CCCAATGTTGCTGTATATCCATTGTCACTGTGTAAGTGTGACTTATGACTTCATC	600
Db	629	CCCAATGTTGCTGTATATCCATTGTCACTGTGTAAGTGTGACTTATGACTTCATC	688
Qy	601	AAGGATGCGCTCCTGAAAGCAACTCATGACAGTGAACCTCCCTTSCCACTTCACTCT	660
Db	689	AAGGATGCGCTCCTGAAAGCAACTCATGACAGTGAACCTCCCTTSCCACTTCACTCT	748
Qy	661	GCTTTGGGAGGCTTCTGCAACACTGTCAATCCGCTCCCTGTAGACAGTGTCAAGAG	720
Db	749	GCTTTGGGAGGCTTCTGCAACACTGTCAATCCGCTCCCTGTAGACAGTGTCAAGAG	808
Qy	721	AGATACATGAACCTCTGCGGAGTACAGTACAGTGCCTGACCTTACCATG	780
Db	809	AGATACATGAACCTCTGCGGAGTACAGTACAGTGCCTGACCTTACCATG	868
Qy	781	CTCCAGAGAGAGGAGCCCGAGACTTCTTACAAAGGTTCAAGGCCCTCTTCCGGTNG	840
Db	869	CTCCAGAGAGAGGAGCCCGAGACTTCTTACAAAGGTTCAAGGCCCTCTTCCGGTNG	928
Qy	841	GGTTCCTGGAACCTGTGTATGTGTGTCACTTATGACAGCTGAAGACCTCTATGGCT	900
Db	929	GGTTCCTGGAACCTGTGTATGTGTGTCACTTATGACAGCTGAAGACCTCTATGGCT	988
Qy	901	GCTGCACTTCCGAGAGGCTCCCTTCTGA 930	
Db	989	GCTGCACTTCCGAGAGGCTCCCTTCTGA 1018	

RESULT 3
US-60-485-450-562
; Sequence 562, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARBELL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01470

CURRENT APPLICATION NUMBER: US/60/485,450
 CURRENT FILING DATE: 2003-07-09
 NUMBER OF SEQ ID NOS: 47859
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 562
 LENGTH: 1617
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-60-485-450-562

Query Match 99.7% Score 927.6; DB 8; Length 1617;
 Best Local Similarity 99.5% Pred. No. 7.6e-257;
 Matches 925; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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 351 ATGGTTGGGTTCAAGGCGCACAGATGTGCCCCCTACTGCACTGTGAAGTTCTTGGGGCT 410
 61 GGCACAGCTGCTGCTGATGCAATCTCACTCTTCTCTGATGACTGCTAAAGTCCGG 120
 411 GGCACAGCTGCTGCTGATGCAATCTCACTCTTCTCTGATGACTGCTAAAGTCCGG 470
 121 TTACAGATCCAGAGGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCCAGCCAGTACCG 180
 471 TTACAGATCCAGAGGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCCAGCCAGTACCG 530
 181 GGTGTGATGGGACCACTTCTGACCATGTGTGCTGCTAGAGGCGCCCGGAGCCTCTCAAT 240
 531 GGTGTGATGGGACCACTTCTGACCATGTGTGCTGCTAGAGGCGCCCGGAGCCTCTCAAT 590
 241 GGGCTGGTTGCGGCGCTGACAGCGCAATGAGCTTTCCTGCTGCTGCTGCTGCTGCTGAT 300
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 361 CTAGCAGGACAGACCAAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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 771 AAGTCCGATTCACAGCTCAGGCGCGGCTGAGGTGCTGAGATACCAAGACCGCTC 830
 481 AATGCTTCAAGACCAATGCTCCGAGAGAGGCTTCCGGGCTCTTGAAAGGAGCCTCT 540
 831 AATGCTTCAAGACCAATGCTCCGAGAGAGGCTTCCGGGCTCTTGAAAGGAGCCTCT 890
 541 CCCAATGTTGCTGTAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 891 CCCAATGTTGCTGTAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 950
 601 AAGATGCTGCTGCTGTAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 951 AAGATGCTGCTGCTGTAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1010
 661 GCGTTGGGGGAGGCTTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 1011 GCGTTGGGGGAGGCTTCTGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
 721 AATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 1071 AATACATGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
 781 CTCACAGAGAGAGGCGCCGAGCTTCTACAAAGGCTTCAATGCTGCTGCTGCTGCTGCTGCT 840
 1131 CTCACAGAGAGAGGCGCCGAGCTTCTACAAAGGCTTCAATGCTGCTGCTGCTGCTGCTGCTG 1190
 841 GGTTCCTGGAAGCTGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 1191 GGTTCCTGGAAGCTGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1250

901 GCGTCACTTCCGAGAGGCTCCCTTCTGA 930
 1251 GCGTCACTTCCGAGAGGCTCCCTTCTGA 1280

RESULT 4

US-60-507-481-2199
 Sequence 2199, Application US/60507481

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL

TITLE OF INVENTION: MODLES OF INFLAMMATORY DISEASES

FILE REFERENCE: AM101084

CURRENT APPLICATION NUMBER: US/60/507,481

CURRENT FILING DATE: 2003-10-02

NUMBER OF SEQ ID NOS: 210107

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2199

LENGTH: 930

TYPE: DNA

ORGANISM: Canis familiaris

US-60-507-481-2199

Query Match 88.2% Score 820.4; DB 8; Length 930;
 Best Local Similarity 92.2% Pred. No. 5e-226;
 Matches 857; Conservative 6; Mismatches 67; Indels 0; Gaps 0;

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 1 ATGGTTGGGTTCAAGGCGCACAGATGTGCCCCCTACTGCACTGTGAAGTTCTTGGGGCT 60
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 61 GGCACAGCTGCTGCTGATGCAATCTCACTCTTCTCTGATGACTGCTAAAGTCCGG 120
 61 GGCACAGCTGCTGCTGATGCAATCTCACTCTTCTCTGATGACTGCTAAAGTCCGG 120
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 121 CTGAGATCCAGAGGAGAAAGTCAGAGGCGCAGTGGCGCTACAGCCAGCCAGTACCG 180
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 601 AAGATGCTGCTGCTGTAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 601 AAGATGCTGCTGCTGTAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

QY 661 GCTTTGGGGGAGGCTTCTGACCACTGTGATGCGCTCCCTGTAGAGCTGTCAAGAG 720
 DB 661 GCTTTCGGGGGAGGCTTCTGACCACTGTGATGCGCTCCCTGTAGAGCTGTCAAGAG 720
 QY 721 AGATACATGAACTCTGCTCCCTGGGCGAGTACAGTACGCTGCGCACTGTGCTTACATG 780
 DB 721 AGATATATGAACTCTGCTCCCTAGGCGAGTACAGTACGCTGCGCACTGTGCTTACATG 780
 QY 781 CTCCAGAGAGAGAGGCGCGGAGGCTTCTTCAAAAGGCTTCAAGCTTCTTCTCCGCTTG 840
 DB 781 CTCCAGAGAGAGAGGCGCGGAGGCTTCTTCAAAAGGCTTCAAGCTTCTTCTCCGCTTG 840
 QY 841 GGTTCCTGGAACCTGTGTGATGTTCTGCACTATGAGAGCTGAAAGAGGCTTCAAGCT 900
 DB 841 GGTTCCTGGAACCTGTGTGATGTTCTGCACTATGAGAGCTTCAAGAGGCTTCAAGCT 900
 QY 901 GCTTGCATCTTCCGAGAGGCTTCCCTTCTGA 930
 DB 901 GCTTGCATCTTCCGAGAGGCTTCCCTTTTAA 930

RESULT 5

US-10-743-643-169
 ; Sequence 169, Application US/10743643
 ; GENERAL INFORMATION:
 ; APPLICANT: Woolf et al.
 ; TITLE OF INVENTION: Nucleic acid and amino acid sequences involved in pain
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/743,643
 ; FILE REFERENCE: 17633/2003-12-22
 ; PRIOR APPLICATION NUMBER: 10/219,051
 ; PRIOR FILING DATE: 2002/07/14
 ; NUMBER OF SEQ ID NOS: 2605
 ; SOFTWARE: perl script
 ; SEQ ID NO 169
 ; LENGTH: 1575
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; DATABASE ACCESSION NUMBER: Refseq / NM_019354
 ; DATABASE ENTRY DATE: 2003-01-13
 ; US-10-743-643-169

Query March 81.9%; Score 762; DB 6; Length 1575;
 Best Local Similarity 88.7%; Pred. No. 4.1e-209;

Matches 825; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 1 ATGGTTGGGTTCAAGGCGACAGATGTGCCCCCTACTGCACTGTGAAGTTCTTGGGCT 60
 DB 345 ATGGTTGGTTCAGAGCGCACCGATGTGCCCCCAACAGCACCGTGAAGTTCTTGGGCT 404
 QY 61 GGCAAGCTGCTGCACTGCGAGATCTGACCTTCCCTGGATCTGCTAAAGTCGG 120
 DB 405 GGGACAGAGCTCTTA-TTGAATCTATCTCTTCCCTTAGACACGGCCAAAGTCCGG 464
 QY 121 TTACAGATCCAGAGAGAAATCAAGGGGCGAGTCCGCGTACAGCCAGCCCAAGTACCGC 180
 DB 465 CTGCAGATCCAGAGAGAGTCAAGGGGCTAGCGCGACCGCGCCAGCCCAAGTACCGC 524
 QY 181 GGTGTGATGGGACACATCTGACCACTGTGCGTACAGAGGGGCGCGGAGGCTTCAACAT 240
 DB 525 GGGGTGTGGGACACATCTTACCATGTGTGCGCTGAGGGTCCGCGAGGCTTCAACAT 584
 QY 241 GGGCTGTGTGGGCTGCAAGCGGCAATGAGCTTTCCTCTGTCGCACTCGGCTGTAT 300
 DB 585 GGGCTGTGTGGGCTGCAAGCGGCAATGAGCTTTCCTCTGTCGCACTCGGCTGTAT 644
 QY 301 GATTCTGCAAAAGTTCTTACACCAAGGGCTTGAAGATCCAGCATTTGGAGCCGCTTC 360
 DB 645 GACTCTGTAAAGAGGTTCTTACACCAAGGGCTTGAAGATCCAGCATTTGGAGCCGCTTC 704
 QY 361 CTAGAGGAGAGACACAGATGCTGCTGTGCTGTGCTGTGCTGAGCCCAAGCATGTGTGTA 420

DB 705 CTGGCAGGTAGACACCAAGGTGCTGCTGCTGTGAGCCCACTACAGATGTGTA 764
 QY 421 AAGTTCGATTCGAAAGTCAAGGCGCGGCTGAGAGTGTGTGAGATACCAAGCACTTC 480
 DB 765 AAGTTCGATTCGAAAGTCAAGGCGCGGCTGAGAGTGTGTGAGATACCAAGCACTTC 824
 QY 481 AATGCTTCAAGACCATTTGCGCGAGAGAGGCTTCCGAGGCTCTGAGAAAGGACCTTC 540
 DB 825 GAGGCTTCAAGACCATTTGCAAGAGAGAGGATCCGAGGCTCTGAGAAAGGACCTTC 884
 QY 541 CCCATGTTGTCTGTAATGCAATGTAATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 600
 DB 885 CCCATGTTGTCTGTAATGCAATGTAATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 944
 QY 601 AAGATGCTCTCTGAAAGCCCACTGATGACAGATGACCTGCTTGCACCTTCACTTCT 660
 DB 945 AAGATGCTCTCTGAAAGCCCACTGATGACAGATGACCTGCTTGCACCTTCACTTCT 1004
 QY 661 GCTTTGGGGGAGGCTTCTGACCACTGTGATGCGCTCCCTGTAGAGCTGTCAAGAG 720
 DB 1005 GCTTTCGGGGGAGGCTTCTGACCACTGTGATGCGCTCCCTGTAGAGCTGTCAAGAG 1064
 QY 721 AGATACATGAACTCTGCTCCCTGGGCGAGTACAGTACGCTGCGCACTGTGCTTACATG 780
 DB 1065 AGATATATGAACTCTGCTCCCTAGGCGAGTACAGTACGCTGCGCACTGTGCTTACATG 1124
 QY 781 CTCCAGAGAGAGAGGCGCGGAGGCTTCTTCAAAAGGCTTCAAGCTTCTTCTCCGCTTG 840
 DB 1125 CTCCAGAGAGAGAGGCGCGGAGGCTTCTTCAAAAGGCTTCAAGCTTCTTCTCCGCTTG 1184
 QY 841 GGTTCCTGGAACCTGTGTGATGTTCTGCACTATGAGAGCTTCAAGAGGCTTCAAGCT 900
 DB 1185 GGTTCCTGGAACCTGTGTGATGTTCTGCACTATGAGAGCTTCAAGAGGCTTCAAGCT 1244
 QY 901 GCTTGCATCTTCCGAGAGGCTTCCCTTCTGA 930
 DB 1245 GCTTGCATCTTCCGAGAGGCTTCCCTTTTGA 1274

RESULT 6

US-60-493-007-1024
 ; Sequence 1024, Application US/604933007
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendrick, Donna
 ; APPLICANT: Porter, Mark
 ; APPLICANT: Johnson, Kory
 ; APPLICANT: Higgins, Brandon
 ; APPLICANT: Castle, Arthur
 ; APPLICANT: Blashoff, Michael
 ; TITLE OF INVENTION: Primary rat hepatocyte toxicity modeling
 ; FILE REFERENCE: 44921-5113-01-US
 ; CURRENT APPLICATION NUMBER: US/60/493,007
 ; PRIOR FILING DATE: 2003-08-07
 ; PRIOR APPLICATION NUMBER: 60/353,171
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: US 60/363,534
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: US 60/371,135
 ; PRIOR FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: US 60/371,134
 ; PRIOR FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: US 60/370,248
 ; PRIOR FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: US 60/371,150
 ; PRIOR FILING DATE: 2002-04-10
 ; PRIOR APPLICATION NUMBER: US 60/371,413
 ; PRIOR FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: US 60/373,601
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/374,139
 ; PRIOR FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: US 60/394,253
 ; PRIOR FILING DATE: 2002-07-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3518
SOFTWARE: Patent Ver. 2.1

SEQ ID NO 1024
LENGTH: 1575

TYPE: DNA
ORGANISM: Rattus norvegicus

FEATURE: Rattus norvegicus
OTHER INFORMATION: Genbank Accession No. AB010743

US-60-493-007-1024

Query Match 81.9%; Score 762; DB 8; Length 1575;
Best Local Similarity 88.7%; Pred. No. 4.1e-209;

Matches 825; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

```

QY 1 ATGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCGCATGTGAAGTTCTTGAGGCT 60
DB 345 ATGTTGGTTTCAAGGCCACAGATGTGCCCCCTACTGCGCATGTGAAGTTCTTGAGGCT 404
QY 61 GGACAGCTGCTGATCGAGATCTCATCACTTTCTCTGATCTGCTAAAGTCCGG 120
DB 405 GGACAGCAGCTGATCTGATCTCATCACTTTCTCTGATCTGCTAAAGTCCGG 464
QY 121 TTACAGATCCAAAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCGCCCAAGTACCG 180
DB 465 CTGCAGATCCAAAGAAAGTCAAGGGCTACAGCGCGCACCGCGCCAGCGCCCAAGTACCG 524
QY 181 GGTGTGATGGGAGCATTCTGACCATGTGTGCTAGTGAAGGCCCGGCAAGCTCTTCAAT 240
DB 525 GCGCTGTGGGAGCATTCTTAAACATGTGTGCGCATGAGGCTCCGCGCAGCTCTTCAAT 584
QY 241 GGGCTGTGTCGGCGCTTCAAGCGCCAAATGAGCTTCTCTGTGCGCATGCGCTGTAT 300
DB 585 GGGCTGTGTCGGCGCTTCAAGCGCCAAATGAGCTTCTCTGTGCGCATGCGCTGTAT 644
QY 301 GATTGTCTCAAGATCTTCAACCAAGGGCTCTGAGATGCGAGCATTTGGAGCGCGCT 360
DB 645 GACTGTGAAGCAGATCTTCAACCAAGGGCTCTGAGATGCGAGCATTTGGAGCGCGCT 704
QY 361 CTAGCAGGACAGCAGCAGGTGCGCTGTGCTGTGCGCCAGCCAGATGTGTA 420
DB 705 CTGCGAGGTAGACACAGGTGCGCTGTGCTGTGCGCCAGCTTACAGATGTGTA 764
QY 421 AAGGTCCGATTTCAAGCTCAGGCGCGGCTGAGTGTGCGAATACCAAGCAGCGCT 480
DB 765 AAGGTCCGCTTCAAGCAGGCGCGGCTGAGTGTGCGAATACCAAGCAGCGCT 824
QY 481 AATGCTTCAAGACCATTTGCGGAGAGAGAGGTTCCGGGCTCTTGAAGAGGACCTCT 540
DB 825 GAAGCTTCAAGACCATTTGCGGAGAGAGAGGTTCCGGGCTCTTGAAGAGGACCTCT 884
QY 541 CCCAATTTGCTGTGAATGCGCATTTGCACTGTGTGAGTGTGAGTGTGAGTGTGAGT 600
DB 885 CCCAATTTGCTGTGAATGCGCATTTGCACTGTGTGAGTGTGAGTGTGAGTGTGAGT 944
QY 601 AAGGATGCGCTTCTGAAAGCCAACTCATGACAGTACCTCCCTTGCACCTTCACTTCT 660
DB 945 AAGGATGCGCTTCTGAAAGCCAACTCATGACAGTACCTCCCTTGCACCTTCACTTCT 1004
QY 661 GCGTTTGGGGGAGGCTTCTGACCATGTATGCGCTTCTCTGTGAGTGTGAGTGTGAGT 720
DB 1005 GCGTTTGGGGGAGGCTTCTGACCATGTATGCGCTTCTCTGTGAGTGTGAGTGTGAGT 1064
QY 721 AAGTACATGAATCTGCGCTTGGGAGTACAGTACGCTGAGCAGTGTGAGTGTGAGT 780
DB 1065 AAGTACATGAATCTGCGCTTGGGAGTACAGTACGCTGAGCAGTGTGAGTGTGAGT 1124
QY 781 CTCAGAGAGAGAGGCGCGGAGCTTTTCAAAAGGTTCAATGCGCTCTTCTTCTCGCTTG 840
DB 1125 CTCAGAGAGAGAGGCGCGGAGCTTTTCAAAAGGTTCAATGCGCTCTTCTTCTCGCTTG 1184
QY 841 GGTTCCTGGAAGTGTGATGTTCGACCTATGAGCAGTGAAGAGAGGCTCATGAGCT 900

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DB 1185 GATCCTGAGACGTAGTAAATGTTTGTCACTTATGACAGCTCAAAAGGCGCTGATGCT 1244
QY 901 GCGTGAAGTCCCGAGAGGCTCCCTTCTGA 930
DB 1245 GCGTGAAGTCCCGAGAGGCGCTTCTTGA 1274

```

RESULT 7

US-60-531-341-500

Sequence 500: Application US/60531341

GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation doing business as Massachusetts Gener

APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nucleotide sequences involved in pain

FILE REFERENCE: 17633/2041

CURRENT APPLICATION NUMBER: US/60/531,341

NUMBER OF SEQ ID NOS: 2587

SOFTWARE: Perl script

SEQ ID NO 500

LENGTH: 1575

TYPE: DNA

ORGANISM: Rattus norvegicus

PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Refseq / NM_019354

DATABASE ENTRY DATE: 2003-10-05

US-60-531-341-500

Query Match 81.9%; Score 762; DB 8; Length 1575;
Best Local Similarity 88.7%; Pred. No. 4.1e-209;
Matches 825; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

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QY 1 ATGTTGGGTTCAAGGCCACAGATGTGCCCCCTACTGCGCATGTGAAGTTCTTGAGGCT 60
DB 345 ATGTTGGTTTCAAGGCCACAGATGTGCCCCCTACTGCGCATGTGAAGTTCTTGAGGCT 404
QY 61 GGACAGCTGCTGATCGAGATCTCATCACTTTCTCTGATCTGCTAAAGTCCGG 120
DB 405 GGACAGCAGCTGATCTGATCTCATCACTTTCTCTGATCTGCTAAAGTCCGG 464
QY 121 TTACAGATCCAAAGAAAGTCAAGGGCCAGTGGCGCTACAGCCAGCGCCCAAGTACCG 180
DB 465 CTGCAGATCCAAAGAAAGTCAAGGGCTACAGCGCGCACCGCGCCAGCGCCCAAGTACCG 524
QY 181 GGTGTGATGGGAGCATTCTGACCATGTGTGCTAGTGAAGGCCCGGCAAGCTCTTCAAT 240
DB 525 GCGCTGTGGGAGCATTCTTAAACATGTGTGCGCATGAGGCTCCGCGCAGCTCTTCAAT 584
QY 241 GGGCTGTGTCGGCGCTTCAAGCGCCAAATGAGCTTCTCTGTGCGCATGCGCTGTAT 300
DB 585 GGGCTGTGTCGGCGCTTCAAGCGCCAAATGAGCTTCTCTGTGCGCATGCGCTGTAT 644
QY 301 GATTGTCTCAAGATCTTCAACCAAGGGCTCTGAGATGCGAGCATTTGGAGCGCGCT 360
DB 645 GACTGTGAAGCAGATCTTCAACCAAGGGCTCTGAGATGCGAGCATTTGGAGCGCGCT 704
QY 361 CTAGCAGGACAGCAGCAGGTGCGCTGTGCTGTGCGCCAGCCAGATGTGTA 420
DB 705 CTGCGAGGTAGACACAGGTGCGCTGTGCTGTGCGCCAGCTTACAGATGTGTA 764
QY 421 AAGGTCCGATTTCAAGCTCAGGCGCGGCTGAGTGTGCGAATACCAAGCAGCGCT 480
DB 765 AAGGTCCGCTTCAAGCAGGCGCGGCTGAGTGTGCGAATACCAAGCAGCGCT 824
QY 481 AATGCTTCAAGACCATTTGCGGAGAGAGAGGTTCCGGGCTCTTGAAGAGGACCTCT 540
DB 825 GAAGCTTCAAGACCATTTGCGGAGAGAGAGGTTCCGGGCTCTTGAAGAGGACCTCT 884
QY 541 CCCAATTTGCTGTGAATGCGCATTTGCACTGTGTGAGTGTGAGTGTGAGTGTGAGT 600
DB 885 CCCAATTTGCTGTGAATGCGCATTTGCACTGTGTGAGTGTGAGTGTGAGTGTGAGT 944
QY 601 AAGGATGCGCTTCTGAAAGCCAACTCATGACAGTACCTCCCTTGCACCTTCACTTCT 660

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Db      324 CTGAGATCCAGGGGGAGAACCAAG---CGGTCCAGACGGCCCGGCTCGTCAATACCGT 380
Qy      181 GGTGTGATGAGGACCACTTGTGACCATGAGTGGAGGGGCCCCGAGAGCCCTACAT 240
Db      381 GGGGTGCTGGGACCACTTGTGACCATGAGTGGAGGGTCTCTGACGAGCCCTTACAT 440
Qy      241 GGGGTGCTGGGACCTGACGAGCCGCAATGAGCTTGGCTCTGTCGCAATCGGCTGTAT 300
Db      441 GGGGTGCTGGGACCTGACGAGCCGCAATGAGCTTGGCTCTGTCGCAATCGGCTGTAT 500
Qy      301 GATTGTGTCAAAAGTTCTACA---CCAGGGGCTCTGAGCATATCCGACATTTGGAGACCCG 357
Db      501 GACTCCGTCAAGCAGGTGTACACCCCAAGGGCGGGACACATTCAGCCTCACTACCCG 560
Qy      358 CTCTAGAGGAGGACGACAGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 417
Db      561 ATTTTGGCCGGCTGACACAGAGGACCATGGCGGTGACCTGTGCCCAAGCCCAAGATGTG 620
Qy      418 GTAAAGTCCGATTCGAAAC-----TCAGGCCCGGGCTGAGGTGTGGAGATAC 468
Db      621 GTGAAGTCCGATTCGAAAC-----TCAGGCCCGGGCTGAGGTGTGGAGATAC 680
Qy      469 CAAGGACCGGCTGACATGCTTACAGAGCCATTCGCGAGAGGAGGAGGAGGAGGAGGAGGAG 528
Db      681 AGCGGACCTATGAGAGGCTTACAGAGCCATTCGCGAGAGGAGGAGGAGGAGGAGGAGGAG 740
Qy      529 AAAGGACCTTCTCCCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db      741 AAAGGACCTTGTCCCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 800
Qy      589 TATGACCTCATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 648
Db      801 TACGACATCTTAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 860
Qy      649 CACTTCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 708
Db      861 CACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 920
Qy      709 GTGTGTGAGAGAGATATCATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 768
Db      921 GTGTGTGAGAGAGATATCATGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 980
Qy      769 GCCCTTACATGCTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
Db      981 ATGATTAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1040
Qy      829 TTTTCTCCGCTTGGGTCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 888
Db      1041 TTTTCTCCGCTTGGGTCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1100
Qy      889 GGCCTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
Db      1101 GGCCTCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1142

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; SEQ ID NO 263
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: predictive genes for liver necrosis
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
PCT-US03-10141-263

Query Match      45.3%   Score 421.4; DB 1; Length 674;
Best local similarity 91.6%   Pred. No. 4,6e-111;
Matches 446; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Db      368 GCAGCACCACAGGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 427
Qy      88 GAGCACCACACAGGTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 147
Db      428 GATTCCAGCTCAGCCCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 487
Qy      148 GCTTCCAGGCTCAGCCCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 207
Db      488 ACAAGACCATTTGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 547
Qy      208 ACAAGACCATTTGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 267
Db      548 TTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 607
Qy      268 TTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 327
Db      608 CCTCTGTAAGGACCACTCATGACAGATACCTCTCTGCACTTCACTTCTGCTTGG 667
Qy      328 CTCTCTGTAAGGACCACTCATGACAGATACCTCTCTGCACTTCACTTCTGCTTGG 387
Db      668 GGGGAGGCTTGTGACACAGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 727
Qy      388 GGGGAGGCTTGTGACACAGTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447
Db      728 TGAATCTGAGCCCTGGGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 787
Qy      448 TGAATCTGAGCCCTGGGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 507
Db      788 AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 847
Qy      508 AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 567
Db      848 GGAACGT 854.
Qy      568 GGAACGT 574
Db

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RESULT 10
PCT-US03-10141-263
; Sequence 263, Application PC/TUS0310141
; GENERAL INFORMATION:
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Uma
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Liver Necrosis Predictive Genes
; FILE REFERENCE: 2874-022PCT
; CURRENT APPLICATION NUMBER: PCT/US03/10141
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/369,287
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0

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RESULT 11
PCT-US03-14832-406
; Sequence 406, Application PC/TUS0314832
; GENERAL INFORMATION:
; APPLICANT: Kier, Larry
; APPLICANT: Nolan, Timothy D.
; APPLICANT: Sankar, Uma
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Liver Inflammation Predictive Genes
; FILE REFERENCE: 2874-023PCT
; CURRENT APPLICATION NUMBER: PCT/US03/14832
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/379,831
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 674
; TYPE: DNA

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RESULT 12
US-10-404-460-263
Sequence 263, Application US/10404460
GENERAL INFORMATION:
APPLICANT: PHASE-I Molecular Toxicology, Inc.
APPLICANT: Kier, Larry
APPLICANT: Nolan, Timothy D.
APPLICANT: Samkar, Usha
APPLICANT: Derbel, Maher
TITLE OF INVENTION: Liver Necrosis Predictive Genes
FILE REFERENCE: 2874-022
CURRENT APPLICATION NUMBER: US/10/404,460
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/369,287
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 263
LENGTH: 674
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Predictive genes for liver necrosis

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QY	366	GGAGACACCAAGAGTACCCTGGCTGTGGCTGTGGCCAGGCCAAGATGTGTAAAGATCC	427
Db	88	GGAGACACCAAGATGCCCTGTGTGTGTGGCCCAACTCAAGATGTGTAAAGATCC	147
QY	428	GATTCCAACTCAGGCCCCGGCTGGAGGTGTGTGAGATATCCAAAGACCTTCATTTGCT	487
Db	148	GCCTCCAGGCCAGGCCCGGGCTGGCGTGTGTGGAGATATCCAGACACTGTTCGAAGCTT	207
QY	488	ACAAGACCTTSCCCGAGAGGAAAGGATTCGGGGGCTCTGSAAGAGGACCTTCCCAATG	547
Db	208	ACAAGACCTTTCAGAGAGAGAAAGGATCCGGGGCTCTGSAAGAGGACCTTCCCAATG	267
QY	548	TTCCTGTATGCACTTGTCAACTGTGTGCTGATGCTGTGACCTATGACTCTATCAAGATG	607
Db	268	TTCGCCGAATGCCATTGTCAACTGTGTACTGAGCTGTGATCATATGACTTCATCAAGATAT	327
QY	608	CCCTCCGTAAGCCAACTCTCAATGACATATACCTCCCTTGCACCTCACTTGTGCCTTGG	667
Db	328	CTCTCTGTAAGCCAACTCTCAATGACATATGACATATGACATATGACATATGACATATG	387
QY	668	GAGCAGGCTTCTGCAACACTGTATCATCGCTTCCTCTGTATGACCTGTGTCAAGAGATATCA	727
Db	388	GAGCAGGCTTCTGCAACAACGCTATTCCTCTCCCATGTATGTGTCAAGAGAGATATCA	447
QY	728	TGAACCTGCTCCCTGGAGCCAGTACAGTATAGCGCTGGCCACTGTGCTCTTACCATGCTCAGA	787
Db	448	TGAACCTGCTCCCTGGAGCCAGTATCAACAGCGCGGGCCACTGTGCTCTTACCATGCTCAGA	507
QY	788	AGGAGGGGCCCCGAGCTTTCTACAAAGGATTCATGCTCTCTTTCTTCGCTTGGGTCTCT	847
Db	508	AGGAGGGGCCCCGAGCTTTCTACAAAGGAGTTCATGCTCTCTTTCTTCGCTTGGGTCTCT	567
QY	848	GGAAGCT 854	
Db	568	GGAAGCT 574	

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Query Match      44.2%; Score 411; DB 5; Length 1133;
Best Local Similarity 70.5%; Pred. No.5,4e-108;
Matches 597; Conservative 0; Mismatches 235; Indels 15; Gaps 3
QY      1 ATGTTGGTTCACGCCACAGATGAGCCCCCTACTGCACGTGGAAGTTTCCTGGGGCT 60
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Db      154 ATGGTTGAGCTGAAGACCTTTCAGACGCTCTCCACCAATGCTGTGAAGTTCTCGGGAGCA 213
Qy      61  GGACAGCTGCTCATGAGATGCTATCACTTCTCTGTGATATCTGTAAAGTCCGG 120
Db      214 GGCACAGAGCTGTTTGTGCTGACCTGTTACCTTTCATGTGACACAGCAAGTCCCG 273
Qy      121 TTAAGATCCAAAGAGAAAGTCAAGGGGCACTGCGCTTACAGCCAGCCCAATACCG 180
Db      274 CTGACATCCAGGGGAGAACAG---CGCTCAGACGGCCCGCTGCTGACGTACCT 330
Qy      181 GGTGTATGGGACCATCTGATCCATAGGTGTGCTGATCAAGGAGCCCGCAAGCTCTACAT 240
Db      331 GCGTGTGGGACCATCTGATCCATAGGTGTGCTGATCAAGGAGCTCTGACCCCTTACAT 390
Qy      241 GGGCTGTGGCGGCTGACAGCGCCAAATGACTTTCCTGTCTGCTGCTGCTGCTGAT 300
Db      391 GGGCTGTGGCGGCTGACAGCGCCAAATGACTTTCCTGTCTGCTGCTGCTGCTGAT 450
Qy      301 GATTCTGTCAAAAGTTCTACA---CCAAAGGCTCTGAGCATGCGCAATGAGGAGCCG 357
Db      451 GACTCTGTAAAGAGGTGTACACCCCAAGGCGGCAACATTCAGCTCACTACCTACCT 510
Qy      358 CTCTAGAGGAGGACACACAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 417
Db      511 ATTTGGCGGCTGACACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 570
Qy      418 GTAAAGTCCGATTCAGAC-----TCAGGCGCGGCTGAGGTGTGAGATATAC 468
Db      571 GTAAAGTCCGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 630
Qy      469 CAAGGACCGTCAATGCTCAAGACCATTCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 528
Db      631 AGCGGAGCATATGAGAGGCTTACAGAACCATGCGGAGGAGGAGGAGGAGGAGGAGG 690
Qy      529 AAAGGACCTCTCCCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
Db      691 AAAGGACCTTTCGCAATCATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 750
Qy      589 TATGACCTCATCAAGAGAGGCTCTGAAAGCAACCTCAATGACAGATGACCTCCCTG 648
Db      751 TACGACATCTCAAGAGAGAGTGTGCTGACCTGCTGCTGCTGCTGCTGCTGCTG 810
Qy      649 CACTTCACTTCTGCTTGGGAGGAGGCTTTCGACCACTGCTGCTGCTGCTGCTGCTG 708
Db      811 CACTTGTCTCTGCTTGGAGCGGCTTCTGTGCTCAAGGTGGGCTCTCCGCTGAGAC 870
Qy      709 GTGTCAAGAGAGATATGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
Db      871 GTGTGAAGAGCCGGTATATGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
Qy      769 GCCCTTACATGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
Db      931 ATGATTAAGATGTGGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 990
Qy      829 TTTCTCC 835
Db      991 TGCCTCC 997

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RESULT 14
US-10-616-865-9

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; Sequence 9 Application US/10616865
; GENERAL INFORMATION:
; APPLICANT: NEWELL, MARTHA K
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASE
; FILE REFERENCE: VO139.70017US00
; CURRENT APPLICATION NUMBER: US/10/616.865
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 09/277,575
; PRIOR FILING DATE: 1999-03-27
; PRIOR APPLICATION NUMBER: US 60/082,250
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/101,580

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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/094,519
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-616-865-9

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Query Match      44.2%; Score 411; DB 6; Length 1132;
Best Local Similarity 70.5%; Pred. No. 5.4e-108;
Matches 597; Conservative 0; Mismatches 235; Indels 15; Gaps 3;

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Qy      1  ATGGTTGAGCTGAAGACCTTTCAGACGCTCTCCACCAATGCTGTGAAGTTCTCGGGAGCA 60
Db      154 ATGGTTGAGCTGAAGACCTTTCAGACGCTCTCCACCAATGCTGTGAAGTTCTCGGGAGCA 213
Qy      61  GGACAGCTGCTCATGAGATGCTATCACTTCTCTGTGATATCTGTAAAGTCCGG 120
Db      214 GGCACAGAGCTGTTTGTGCTGACCTGTTACCTTTCATGTGACACAGCAAGTCCCG 273
Qy      121 TTAAGATCCAAAGAGAAAGTCAAGGGGCACTGCGCTTACAGCCAGCCCAATACCG 180
Db      274 CTGACATCCAGGGGAGAACAG---CGCTCAGACGGCCCGCTGCTGACGTACCT 330
Qy      181 GGTGTATGGGACCATCTGATCCATAGGTGTGCTGATCAAGGAGCCCGCAAGCTCTACAT 240
Db      331 GCGTGTGGGACCATCTGATCCATAGGTGTGCTGATCAAGGAGCTCTGACCCCTTACAT 390
Qy      241 GGGCTGTGGCGGCTGACAGCGCCAAATGACTTTCCTGTCTGCTGCTGCTGCTGAT 300
Db      391 GGGCTGTGGCGGCTGACAGCGCCAAATGACTTTCCTGTCTGCTGCTGCTGCTGAT 450
Qy      301 GATTCTGTCAAAAGTTCTACA---CCAAAGGCTCTGAGCATGCGCAATGAGGAGCCG 357
Db      451 GACTCTGTAAAGAGGTGTACACCCCAAGGCGGCAACATTCAGCTCACTACCTACCT 510
Qy      418 GTAAAGTCCGATTCAGAC-----TCAGGCGCGGCTGAGGTGTGAGATATAC 468
Db      571 GTAAAGTCCGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 630
Qy      589 TATGACCTCATCAAGAGAGGCTCTGAAAGCAACCTCAATGACAGATGACCTCCCTG 648
Db      751 TACGACATCTCAAGAGAGAGTGTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 810
Qy      649 CACTTCACTTCTGCTTGGGAGGAGGCTTTCGACCACTGCTGCTGCTGCTGCTGCTG 708
Db      811 CACTTGTCTCTGCTTGGAGCGGCTTCTGTGCTCAAGGTGGGCTCTCCGCTGAGAC 870
Qy      709 GTGTCAAGAGAGATATGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
Db      871 GTGTGAAGAGCCGGTATATGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
Qy      769 GCCCTTACATGCTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 828
Db      931 ATGATTAAGATGTGGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 990
Qy      829 TTTCTCC 835

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Db 991 TGCCTCC 997

RESULT 15
US-10-743

US-10-743-643-1711

; Sequence 171, Application US/10743643

GENERAL INFORMATION:

APPLICANT: Woolf et al.

TITLE OF INVENTION: Nucleic acid and amino acid sequences involved in pain

FILE REFERENCE:

FILE REFERENCE: CTRBNT APPLICATION NUMBER: IIS/10/743.643

CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2003-12-22

CURRENT FILING DATE: 2003-12-22
 CIT REFERENCE: 17633/2005

FILE REFERENCE: 17633/2005

PRIOR APPLICATION NUMBER: 10/219,051

PRIOR FILING DATE: 20

NUMBER OF SEQ

SOFTWARE: Per

SOFTWARE: ;
; SEO ID NO 1

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; SEQ ID NO 1/1
;
LENGTH: 1182

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LENGTH: 1182
TYPE: DNA

TYPE: DNA
ORGANISM: Homo sapiens

ORGANISM: Homo

! DATABASE ENTRY DATE: 2001-03-09
US-10-743-643-171

QY	ATGGTGTGGGTTCAAGGCGACAAGATGTGGCCCCCTACTGTGCACATGTGAAGTTCTTTGGAGGCT	60
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Db	GGCACAGCTGCTCGCATCGCAGATCTTCATACACTTCTCTGATGACTGTAAAGTCCGG	264
QY	GGCACAGCAGCTGCTGTTTGTGTGCTCTGTACTTTCACATGACACAGCCGAGTCCGC	121
Db	GGCACAGCAGCTGCTGTTTGTGTGCTCTGTACTTTCACATGACACAGCCGAGTCCGC	324
QY	TTACAGATCCAGAGAAAGTACAGGGGCGAGGCGCGCTACAGCAGCAGGCCAGTACCG	180
Db	TTACAGATCCAGAGAAAGTACAGGGGCGAGGCGCGCTACAGCAGCAGGCCAGTACCG	324
QY	GCTGTGATGGGACATCTTGACCATGTGGCGTACTGAGGGGCGCCGCCAAGGCTCTCAAT	181
Db	GCTGTGATGGGACATCTTGACCATGTGGCGTACTGAGGGGCGCCGCCAAGGCTCTCAAT	361
QY	GCGGTGCTGGGACCAATCTTGACCAATGGTGCGGACTGAGGGTCTTGACGCCCTTCAAT	241
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QY	GGGCTGGTTGGCCGCTCGACGCGCCAAATAGCTTTGCTCTGTCCGATCGGCTGTAT	300
Db	GGGCTGGTTGGCCGCTCGACGCGCCAAATAGCTTTGCTCTGTCCGATCGGCTGTAT	441
QY	GATTCGTGCAACAAGTTCTTACA---CCAAAGGGTCTGAGCATGCGAGCATTGGAGGCGC	301
Db	GATTCGTGCAACAAGTTCTTACA---CCAAAGGGTCTGAGCATGCGAGCATTGGAGGCGC	501
QY	GACTCGCTGAAAGCAGGTGTACACCCCGAAGGCGCGGACAACTCCAGGCTCAGTACCCGG	358
Db	GACTCGCTGAAAGCAGGTGTACACCCCGAAGGCGCGGACAACTCCAGGCTCAGTACCCGG	561
QY	CTCCTAGCAGGCGACGACCAACGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	417
Db	CTCCTAGCAGGCGACGACCAACGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	561
QY	ATTTTGGCGGCTCAGCACCAGGAGGCCATGGCGGTGTAACCTGTGCCCAGCCCAAGAGTGT	418
Db	ATTTTGGCGGCTCAGCACCAGGAGGCCATGGCGGTGTAACCTGTGCCCAGCCCAAGAGTGT	621
QY	GTTAAAGTCCGATTTCCAGC-----TCAGGCGCGGCGTGAAGTGTGCGAGATAC	468
Db	GTTAAAGTCCGATTTCCAGC-----TCAGGCGCGGCGTGAAGTGTGCGAGATAC	621
QY	GTTAAAGTCCGATTTCCAGC-----TCAGGCGCGGCGTGAAGTGTGCGAGATAC	469
Db	GTTAAAGTCCGATTTCCAGC-----TCAGGCGCGGCGTGAAGTGTGCGAGATAC	681
QY	CAAAGCAGCTGCAATGCTCTACAGACCATTTGCCGAGAGAAAGGTTCCGGGGGCTCTGG	528
Db	CAAAGCAGCTGCAATGCTCTACAGACCATTTGCCGAGAGAAAGGTTCCGGGGGCTCTGG	681
QY	AAGCGGAGCTTAAAGACGCTTACAGAACCATGCGAGGAGAAAGGATAGAGGGGCTGTGG	529
Db	AAGCGGAGCTTAAAGACGCTTACAGAACCATGCGAGGAGAAAGGATAGAGGGGCTGTGG	741
QY	AAAGGACGCTCTCCCAATGTGTGCTGTATGCGTATGTCATTTGATCTGATGTAGTGGTAAAC	588
Db	AAAGGACGCTCTCCCAATGTGTGCTGTATGCGTATGTCATTTGATCTGATGTAGTGGTAAAC	741
QY	AAAGGACGCTCTCCCAATGTGTGCTGTATGCGTATGTCATTTGATCTGATGTAGTGGTAAAC	589
Db	AAAGGACGCTCTCCCAATGTGTGCTGTATGCGTATGTCATTTGATCTGATGTAGTGGTAAAC	801
QY	TATGACCTCATTAAGATGCGCTCTCTGAAAGCCAACTCATACAGATGATCCTCCCTTGC	648
Db	TATGACCTCATTAAGATGCGCTCTCTGAAAGCCAACTCATACAGATGATCCTCCCTTGC	801
QY	TATGACCTCATTAAGATGCGCTCTCTGAAAGCCAACTCATACAGATGATCCTCCCTTGC	801
Db	TATGACCTCATTAAGATGCGCTCTCTGAAAGCCAACTCATACAGATGATCCTCCCTTGC	801

Accession	Sequence	Position
QY	GTGGTCAGAGCAGATACATGAACCTCTGCCCTGGGCGAGTACAGTAGCGCGGTGGCCACTCTGT	768
Db	GTGGTCAGAGCAGCGGTATATGAATCTACCTCCAGGCGAGTACTTACAGGCCCTCCACACTGT	980
QY	GCCCTTACCATCTCCAGAGAGAGGGGCCCGGAGCCTTCTACAAAGGGTTATAGCCCTCC	828
Db	ATGATTAAGATGTGTGCCCGAGAGAGGCCCAACAGCCTTCTACAGGGGTGAGCCTCTCC	1040
QY	TTTCTCC 835	
Db	TGCTCTCC 1047	

Search completed: February 4, 2004, 20:16:37
Job time : 415 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 4, 2004, 17:52:58 / Search time 2412 Seconds

(without alignments) 9371.129 Million cell updates/sec

Title: US-09-884-814-2

Sequence: 1 atgctgggtcctcaggccac.....cccgaggctccctcctcga 930

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Listing first 45 summaries

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EST:
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estro:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estom:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	781.2	84.0	3641	11	AK054060 Mus muscu
2	779.6	83.8	3964	11	AK035298 Mus muscu
3	731.4	78.6	782	10	BF974251 BF974251
4	725	78.0	807	10	BF974251 BF974251

5	702.6	75.5	739	14	CA944705	CA944705 UT-CR-FNO
6	702.2	75.5	932	12	B1258707	B1258707 B02965874
7	644.2	73.6	752	12	BM015784	BM015784 603642048
8	672.8	72.3	927	12	B1246501	B1246501 6029292916
9	672.4	72.3	1201	9	AL542338	AL542338 AL542338
10	659	70.9	1201	9	AL581378	AL581378 AL581378
11	652.4	70.2	938	12	B1692548	B1692548 603343091
12	647.6	69.6	1125	9	AL575087	AL575087 AL575087
13	640.6	68.9	859	10	BF976529	BF976529 602244382
14	635.4	68.3	892	12	B1904624	B1904624 603166439
15	634.6	68.2	1201	9	AL552524	AL552524 AL552524
16	633.8	68.2	1073	9	AL555585	AL555585 AL555585
17	630.6	67.8	650	9	AL133329	AL133329 HA1932_Hu
18	630.6	67.8	1201	9	AL535374	AL535374 AL535374
19	626	67.3	709	10	BG284068	BG284068 602407385
20	624	67.1	1167	13	BX421118	BX421118 BX421118
21	618	66.5	766	12	BG976754	BG976754 602845813
22	617.2	66.4	1201	9	AL516805	AL516805 AL516805
23	616.4	66.3	644	12	BG825731	BG825731 602747049
24	613.4	66.0	997	13	BX343473	BX343473 BX343473
25	610.8	65.7	1065	10	BG754934	BG754934 602711629
26	609.6	65.5	753	10	BE513450	BE513450 601316120
27	608.6	65.4	754	10	BG340587	BG340587 602462157
28	606.2	65.2	794	12	BG968126	BG968126 602635587
29	603.4	64.9	1201	13	BX375133	BX375133 BX375133
30	602.6	64.8	1201	9	AL559843	AL559843 AL559843
31	600.8	64.6	882	13	BX384593	BX384593 BX384593
32	596.6	64.2	701	9	AL143017	AL143017 me41808.Y
33	594.6	63.9	1060	9	AL555584	AL555584 AL555584
34	594.4	63.9	896	10	BG341258	BG341258 602463324
35	594	63.9	995	13	BX343474	BX343474 BX343474
36	590.4	63.5	592	10	BE514976	BE514976 601317285
37	589.2	63.4	905	10	BF581001	BF581001 602100115
38	586.8	63.1	1177	12	B0050380	B0050380 AGENCOURT
39	583.2	62.7	684	14	CB446089	CB446089 697877.MA
40	580.8	62.5	1201	9	AL563224	AL563224 AL563224
41	580.4	62.4	1196	9	AL562228	AL562228 AL562228
42	579.4	62.3	859	12	BG972368	BG972368 602841319
43	576.2	62.0	697	12	BG965001	BG965001 602831635
44	576.2	62.0	818	12	B1904048	B1904048 603165559
45	572.2	61.5	1201	9	AL516806	AL516806 AL516806

ALIGNMENTS

RESULT 1	AK054060	3641 bp	mRNA	linear	HTC 05-DEC-2002
LOCUS	AK054060				
DEFINITION	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:1E2300.5118 Product:uncoupling protein 2, mitochondrial, full insert sequence.				
ACCESSION	AK054060.1	GI:26343968			
VERSION	AK054060.1				
KEYWORDS	HTC, CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				

REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagacka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, Y., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, K., Inoue, Y., Kita, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PubMed	11076861
REFERENCE AUTHORS	4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Aachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamahata, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Pleischmann, W., Gassterland, T., Gissi, C., King, B., Kochiwa, H., Kueh, P., Lewis, S., Matsuo, Y., Nakai, I., Pease, G., Tomita, M., Quackenbush, J., Schriml, L. M., Stadhil, F., Suzuki, R., Tomita, M., Wagner, E., Washio, T., Sakai, K., Okido, T., Furuno, W., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Wetz, C., Whitaker, C., Wilming, L., Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PubMed	11217851
REFERENCE AUTHORS	5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	12107851
PubMed	12107851
REFERENCE AUTHORS	6 (bases 1 to 3641) Aachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, P., Imokawa, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (15-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/ Location/Qualifiers

source	1..3641 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM:DB:E230015118" /db_xref="taxon:10090" /clone="E230015118" /sex="female" /tissue_type="ovoiduct" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="2 days pregnant adult"
CDS	369..1298 /note="unnamed protein product; putative uncoupling protein 2, mitochondrial (MGD [MG1:109354, GI NM_011671, evidence: BLASTN, 100%, match=1100])" /codon_start=1 /protein_id="BAC35641.1" /db_xref="GI:26343969" /translation="MVGKATDVPPTATYKFLGACNACINDLIPPLDPAVRPIQIO GESQIVRTASAGYRGLVLTITLWRTSRLNGLVAGLQROMSPASVRIGLYS VKQFYTGSEHAGISRLLAGSTTGALAVVAQPTVVRVRFQAOQAGGRYOSTV EAYKTIAREBIRGLMGTSPNVAARVACALVYVDIKITLKNLMTDLPCH TSARGAGCTVIASPDVYKTRMSALGQYSHGICALTMLRKEGPAPAFYKFWPS FLRIGSNVWVFVTEQLKALMAAYSRAP"
BASE COUNT	791 a 1075 c 934 g 841 t
ORIGIN	
Query Match	84.0%; Score 781.2; DB 11; Length 3641;
Best Local Similarity	90.0%; Pred. No. 5.2e-189;
Matches 827; Conservative	0; Mismatches 93; Indels 0; Gaps 0;
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489	CTGCAATCCAGAGAGAGTCAAGGCTGATGCGACCGGCGGCGGCGGCGG 548
181	GGTGTATGGGACCATCTGTCAGATGCTGCTGCTGCTGCTGCTGCTGCT 240
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609	GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
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849	GAAGCTCAACAGCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
541	CCCAATGCTGCTGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
909	CCCAATGCTGCTGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 968
601	AAGATGCTGCTGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

Db AAAGATACCTCTCTGAAAGCCAAAGCCATGACAGATGACCTCCCTTGCACATTCATCTT 1028

Qy 661 GCCTTTGGGGAGGCTTGTGACACATGATGATGCGCCCTCTTACAGGTGGACAGAG 720

Db 1029 GCGTTGGGGGCGGCTTGTGACACACGATGCGCTTCCCTTTGATGTGTGTGACAGAG 1088

Qy 721 AGATACATGAATCTGCTGCGGAGGAGTACAGTACGCGTGGCCATGCTGCGCTTACATG 780

Db 1089 AGATACATGAATCTGCGCTTGGGACAGACAGCGCAGGTCACTGTGCGCTTACCATG 1148

Qy 781 CTCACAGAGAGGGGGGCGGAGCTTCTACAAAGGTTGATGCGCTTCTTCCGCTTG 840

Db 1149 CTCGGAGAGAGGGGCGGCGGCTTCTACAAAGGTTGATGCGCTTCTTCCGCTTG 1208

Qy 841 GATTCCTGGAACGTGTGATGTTGATGATGACCTATGAGCAGCTGAAGAGCCCTCATGAGCT 900

Db 1209 GGATCCTGGAACGTGTGATGTTGATGATGACCTATGAGCAGCTGAAGAGCCCTCATGAGCT 1268

Qy 901 GCTTGCACCTTCCCGAGAGGCTTCCCTTCTGA 930

Db 1269 GCTTGCACCTTCCCGAGAGGCTTCCCTTCTGA 1298

RESULT 2
AK035298
LOCUS
DEFINITION
AK035298 3964 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:953001110 product:uncoupling protein 2,
mitochondrial, full insert sequence.

ACCESSION
AK035298 1 GI:26330581
VERSION
AK035298.1
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
MEDLINE
PUBMED
20499374
11042159

TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PUBMED
20499374
11042159

REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (11), 1757-1771 (2000)

TITLE
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
20530913
11076861

REFERENCE
4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arikawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R.,
Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, T., Pesole, G.,
Quackenbush, J., Schriml, L. M., Stabili, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,

Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Butt, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombere, P., Nordone, P.,
Rings, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schombach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyo-Oka, K., Wang, K. H., Weitz, C., Whitaker, C., Williams, J.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsuke, S.
and Hayashizaki, Y.

TITLE
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

JOURNAL
MEDLINE
PUBMED
21085660
11217851

REFERENCE
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
6 (Bases 1 to 3964)
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saito, H., Sakai, K., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
Direct Submission
Submitted (16-UTL-2001) Yoshinori Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://lancom.gsc.riken.go.jp/.
Location/Qualifiers

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/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="953001110"
/sex="male"
/tissue_type="urinary bladder"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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/note="unlabeled protein product; putative
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GB|NM_01671, evidence: BLASTN, 100%, match=1100]"
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/db_xref="GI:26330582"
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EAYTTIRERISRLGKTSPPNRRNIVCALVYDIDIKDILLKRNITDDEPHF
TSRAGAGCTTIVASPDVAVTRVYNSALGOYSHAGCALTWLRKEGPRPFTKGFPS

BASE COUNT 861 a 1158 c 1021 g 904 t
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 ORIGIN

Query Match 83.8%; Score 779.6; DB 11; Length 3964;
 Best Local Similarity 89.9%; Pred. No. 1.4e-188;
 Matches 836; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

1 ATGGTTGGTTCAAGGCAAGATGTCCTTACTGCTGAGCTGTAAGTTTCTGGGCT 60
 363 ATGGTTGGTTCAAGGCAAGATGTCCTTACTGCTGAGCTGTAAGTTTCTGGGCT 422
 61 GGCACAGCTGCTGCAATCGCAATCTCACTTCTCTGTAATCTGTAATCTGGG 120
 423 GGCACAGCTGCTGCAATCGCAATCTCACTTCTCTGTAATCTGTAATCTGGG 482
 121 TTACAGATCCAGAGAGAGTCAAGGAGGAGTGGGCTGACAGAGGAGGAGTACCG 180
 483 CTGCAATCCAGAGAGAGTCAAGGAGGAGTGGGCTGACAGAGGAGGAGTACCG 542
 181 GGTGTGATGGGACCAATCTGACCAATGTCGTAATCTGAGAGGAGGAGGAGTAC 240
 543 GGCCTTCTGGGATCAATCTGACCAATGTCGTAATCTGAGAGGAGGAGTAC 602
 241 GGCCTTCTGGGATCAATCTGACCAATGTCGTAATCTGAGAGGAGGAGTAC 300
 603 GGCCTTCTGGGATCAATCTGACCAATGTCGTAATCTGAGAGGAGGAGTAC 662
 301 GATTCTGTCAAAAGCTTCAACCAAGGAGTCTGACCAATGTCGTAATCTGAGAG 360
 663 GATTCTGTCAAAAGCTTCAACCAAGGAGTCTGACCAATGTCGTAATCTGAGAG 722
 361 CTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 723 CTGCAAGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 782
 421 AAGGTCCGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
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 843 GAAGCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 902
 541 CCAATGTTGCTGTAATGCAATGTCGTAATGTCGTAATGTCGTAATGTCGTAATGTC 600
 903 CCAATGTTGCTGTAATGCAATGTCGTAATGTCGTAATGTCGTAATGTCGTAATGTC 962
 601 AAGATGCTGCTGTAATGCAATGTCGTAATGTCGTAATGTCGTAATGTCGTAATGTC 660
 963 AAGATGCTGCTGTAATGCAATGTCGTAATGTCGTAATGTCGTAATGTCGTAATGTC 1022
 661 GCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
 1023 GCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1082
 721 AGATTCATGAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 1083 AGATTCATGAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1142
 781 CTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
 1143 CTCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1202
 841 GGTTCCTGAAAGTGTGATGTTGCTCACTATGAGCAAGCTGAAAGAGGAGGAGGAGGCT 900
 1203 GGTTCCTGAAAGTGTGATGTTGCTCACTATGAGCAAGCTGAAAGAGGAGGAGGAGGCT 1262
 901 GGTTCCTGAAAGTGTGATGTTGCTCACTATGAGCAAGCTGAAAGAGGAGGAGGAGGCT 930
 1263 GGTTCCTGAAAGTGTGATGTTGCTCACTATGAGCAAGCTGAAAGAGGAGGAGGAGGCT 1292

RESULT 3
 BF974251 782 bp mRNA linear EST 22-JAN-2001
 LOCUS 602243895F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335167 5',
 DEFINITION mRNA sequence.

ACCESSION BF974251
 VERSION BF974251.1 GI:12341466
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 782)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@b-remail.nih.gov

AUTHORS Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LNCM1205 row: m column: 24

FEATURES
 source High quality sequence stop: 780.
 Location/Qualifiers

1..782

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4335167"

/issue_type="Primary B-cells from tonsils (cell line)"

/lab_host="PH10B (phage-resistant)"

/clone_id="NIH MGC 48"

/notes="Torgan: B-cells; Vector: pORF7; Site: 1; XhoI;
 Site: 2; EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACAG(G). Size-selected 500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH-MGC library."

BASE COUNT 159 a 239 c 219 g 165 t

ORIGIN

Query Match

Best Local Similarity 78.6%; Score 731.4; DB 10; Length 782;
 Matches 743; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

55 GGGGCTGGGACAGCTGCTGCAATCGCAATCTCACTTCTCTGTAATCTGTAATCTGTA 114
 2 GGGGCTGGGACAGCTGCTGCAATCGCAATCTCACTTCTCTGTAATCTGTAATCTGTA 61
 115 GTCCGGTTACATTCGA- GGAAGAAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGG 173
 62 GTCCGGTTACATTCGAAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 121
 174 GTACCGGGGTGTGATGGGACCAATTTGACATGCTGTAATGAGGAGGAGGAGGAGGAG 233
 122 GTACCGGGGTGTGATGGGACCAATTTGACATGCTGTAATGAGGAGGAGGAGGAGGAG 181
 234 CTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 293
 182 CTACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
 294 CTTGTATGATTTCTGTCAACAGTCTTACACCAAGGAGGAGGAGGAGGAGGAGGAGGAG 353
 242 CTTGTATGATTTCTGTCAACAGTCTTACACCAAGGAGGAGGAGGAGGAGGAGGAGGAG 301
 354 CCGGCTCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 413

Db	302	CCGCCTCTCAGAGGACACACCAAGAGTCCCTTGCTGTGTGCTGTGTGCCCACTCCACGGA	361
QY	414	TGTGTAAAGSTCCGATTCCAAGCTCAGGCCCGGGCTGGAGGTGTTCGAGATACCAAG	473
Db	362	TGTGTAAAGSTCCGATTCCAAAGCTCAGGCCCGGGCTGGAGGTGTTCGAGATACCAAG	421
QY	474	CACCGTCATGTGCTTACAAGACCATTTGCCCGAGAGAAAGGTTCGGGGCTCTGGAAAAG	533
Db	422	CACCGTCATGTGCTTACAAGACCATTTGCCCGAGAGAAAGGTTCGGGGCTCTGGAAAAG	481
QY	534	GACCTCTCCAAATGTTGCTCGTAATGCATATGTCAACTGTGTGAAGCTGATCACTTGA	593
Db	482	GACCTCTCCCAATGTTGCTCGTAATGCATATGTCAACTGTGTGAAGCTGATCACTTGA	541
QY	594	CCTCATCAAGATGCCCTCTGAAAAGCAACCTCATGACAGATGACCTTCCCTTGCCACTT	653
Db	542	CCTCATCAAGATGCCCTCTGAAAAGCAACCTCATGACAGATGACCTTCCCTTGCCACTT	601
QY	654	CACCTCTGCTTTGGGGCAGGCTTTTGACACACAGTATATGCGCTCCCGTATGAGTGTG	713
Db	602	CACCTCTGCTTTGGGGCAGGCTTTTGACACACAGTATATGCGCTCCCGTATGAGTGTG	661
QY	714	CAGAGAGAGTACATGAACCTGCGCTGGGCGACATGACAGTACGTGGCCACTGTGSCCT	773
Db	662	CAGAGAGAGTACATGAACCTGCGCTGGGCGACATGACAGTACGTGGCCACTGTGSCCT	721
QY	774	TACCATGCTCCAGAAAGGAGGGCCC	798
Db	722	TACCATGCTCCAGAAAGGAGGGCCC	746

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FEATURES
SOURCE
1. 807

LOCUS
807 bp mRNA linear EST 15-MAY-2001

DEFINITION
6027144886F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4855077 5',
mRNA sequence.

ACCESSION
BG757774

VERSION
BG757774

KEYWORDS
EST.

SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 807)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LCM1703 row: 1 column: 22
High quality sequence drop: 788.

LOCATION/Qualifiers
1. 807

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/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI. cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGCACGAC(G). Size-selected
for average insert size 1.8kb. Library constructed by ligation

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BASE COUNT      151 a      255 c      214 g      187 t
ORIGIN
      Hong in the laboratory of Gerald M. Rubin (University of
      California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies).
      Note: this is a NIH-MGC library.
Query Match      78.0% ; Score 725 ; DB 10 ; Length 807 ;
Best Local Similarity 99.9% ; Pred. No. 5.9e-175 ;
Matches 726 ; Conservative 0 ; Mismatches 0 ; Indels 1 ; Gaps 1

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QY	254	GCGTCGAGGCGCAATATGAGCTTTTGCTCTGTTCGCAATGCGAGCTGATGATTTCTGTCAAC	313					
DB	62	GCGTCGAGGCGCAATATGAGCTTTTGCTCTGTTCGCAATGCGAGCTGATGATTTCTGTCAAC	121					
QY	314	AGTTCTACACCAAGGCTCTGAGCANTCCAGATTGGAGCCGCTCTTACAGAGCAGCA	373					
DB	122	AGTTCTACACCAAGGCTCTGAGCATCCAGATTGGAGCCGCTCTTACAGAGCAGCA	181					
QY	374	CCACAGATGTCCTGGCTGTGGCTGTGGCCCAAGCCACAGATGTGGTAAAGGTCGATCC	433					
DB	182	CCACAGATGTCCTGGCTGTGGCTGTGGCCCAAGATGTGGTAAAGGTCGATCC	241					
QY	434	AGACTAGGCGCGGCTGAGATGATGAGATACCAAGACCCGTCAATGGCTACAGA	493					
DB	242	AGACTAGGCGCGGCTGAGATGATGAGATACCAAGACCCGTCAATGGCTACAGA	301					
QY	494	CCATTGCGCGGAGGAGGATTCGGGAGCTCTTGAAAAGGACCTTCCCAATGTTGTC	553					
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QY	614	TGAAGCCACACTCATGACAGTGAACCTCCCTTGCCAATTCACTTGTGCTTGGGAG	673					
DB	422	TGAAGCCACACTCATGACAGTGAACCTCCCTTGCCAATTCACTTGTGCTTGGGAG	481					
QY	674	GCTTCTTGACCACTGTCACTGCTTCCTCTGTAAGCTGTGCAAGAGATACATGAAT	733					
DB	482	GCTTCTTGACCACTGTCACTGCTTCCTCTGTAAGCTGTGCAAGAGATACATGAAT	541					
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DB	542	CTGCGCGGAGCAGTACAGTACGCTGGCCACTGTGCTTACATGCTCCAGAGAGAG	601					
QY	794	GCGCCGAGGCTTTACAAAGGATCATGCCCTCTTTCTTCGCTTGGGTTCTTGAGAG	853					
DB	602	GCGCCGAGGCTTTACAAAGGATCATGCCCTCTTTCTTCGCTTGGGTTCTTGAGAG	661					
QY	854	TGATGATGTCGTCACTATGAGCAGCTGAAAGAGCCCATGAGGCTGCTGACTTCC	913					
DB	662	TGATGATGTCGTCACTATGAGCAGCTGAAAGAGCCCATGAGGCTGCTGACTTCC	720					
QY	914	GAGAGGCTCCTCTGA 930						
DB	721	GAGAGGCTCCTCTCTGA 737						

RESULT 5	
C9A94705/c	
LOCUS	
DEFINITION	739 bp mRNA linear EST 30-DEC-2002
ACCESSION	U9-CF-FNO-aff-m-14-O-U1.s1 UI-CF-FNO Homo sapiens cDNA clone
VERSION	U9-CF-FNO-aff-m-14-O-U1.3', mRNA sequence.
KEYWORDS	C9A94705
SOURCE	C9A94705.1 GI:27433185
	EST.
	Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PubMed 8889548
 COMMENT Contact: McCray, PB
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 Seq primer: M13 FORWARD
 POLYA-yes.

FEATURES
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 /db_xref="taxon:9606"
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 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_id="UI-CF-FNO"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-FNO is a subtracted cDNA library derived from two
 normalized Human lung epithelial cell libraries (EM1 and
 DUL) The library was subtracted according to according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. For additional information, contact:
 bento-soares@uiowa.edu
 TAG_Lib=UI-CF-FNO
 TAG_Tissue=Human Lung Epithelial Cell Lines untreated LPS
 6hr to LPS 24h
 TAG_SBO=CTGCTCAGGT"

BASE COUNT 155 a 197 c 223 g 163 t 1 others
 ORIGIN
 Query Match 75.5%; Score 702.6; DB 14; Length 739;
 Best local similarity 97.9%; Pred. No. 3.1e-169;
 Matches 711; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 160 AGAGCAGCGCCGACGACGCGGGGTGATGAGGACCACTTGTGACCTGCTGCTAGG 219
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 QY 340 GCCAGCATTTGGAGAGCGCTCTCTGACAGGAGCAGCAGAGTGGCTGCTGCTGCTGCT 399
 Db 559 GCCAGCATTTGGAGAGCGCTCTCTGACAGGAGCAGCAGAGTGGCTGCTGCTGCTGCT 500
 QY 400 GCCAGCGCCAGCGAGTGTGAAGGTCCGATTCAGAGCTCAGGCCCGGCTGAGAGTGGT 459
 Db 499 GCCAGCGCCAGCGAGTGTGAAGGTCCGATTCAGAGCTCAGGCCCGGCTGAGAGTGGT 440

QY 460 CGAGATACCAAGACCGCTCATGCTTACAGACCAATGCCCGAGAGAGGATTCGG 519
 Db 439 CGAGATACCAAGACCGCTCATGCTTACAGACCAATGCCCGAGAGAGGATTCGG 380
 QY 520 GGCCTCTGGAAGGAGACCTCTCCCAATGCTGCTGTATATGCCATTTGCACTGCTGAG 579
 Db 379 GGCCTCTGGAAGGAGACCTCTCCCAATGCTGCTGTATATGCCATTTGCACTGCTGAG 320
 QY 580 CTGTGACCTTATGACCTCATCAAGATGCCCTCTGAAAGCAACCTCATGACAGATGAC 639
 Db 319 CTGTGACCTTATGACCTCATCAAGATGCCCTCTGAAAGCAACCTCATGACAGATGAC 260
 QY 640 CTCCTTGGCACTTCACTTCTGCTCTTGGGCGAGGCTTTGCAACATGTCATGCTCC 699
 Db 259 CTCCTTGGCACTTCACTTCTGCTCTTGGGCGAGGCTTTGCAACATGTCATGCTCC 200
 QY 700 CCTGTAGACGTGTGCAAGACGATATCATGAACTCTGCGGCGAGTACAGTACGCT 759
 Db 199 CCTGTAGACGTGTGCAAGACGATATCATGAACTCTGCGGCGAGTACAGTACGCT 140
 QY 760 GGCACTGTGCTCCCTTACCATGCTCTCCAGAGAGGAGGCGCCGAGCTTTCAAGAGGCTTC 819
 Db 139 GGCACTGTGCTCCCTTACCATGCTCTCCAGAGAGGAGGCGCCGAGCTTTCAAGAGGCTTC 80
 QY 820 ATGCCCTCTCTTCTCCGCTTGGGTTCTGGAACGTTGATGTCGTCACCTATGACAG 879
 Db 79 ATGCCCTCTCTTCTCCGCTTGGGTTCTGGAACGTTGATGTCGTCACCTATGACAG 20
 QY 880 CTGAAA 885
 Db 19 CAAAA 14

RESULT 6
 B1258707
 LOCUS
 DEFINITION
 602969874F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109050 5',
 mRNA sequence.
 B1258707
 ACCESSION
 B1258707.1 GI:14815328
 VERSION
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 932)
 AUTHORS NIH-MGC http://imgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 http://image.llnl.gov
 Plate: L1AM1264 row: d column: 19
 High quality sequence stop: 799.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5109050"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_id="NIH MGC 12"
 /note="Organ: cervix; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life

Db 531 AATGCTACAAAGACCAATGCCCCAGAGAGAGGATCCGGGCTCTGAAAGAGGACCTCT 590
 541 CCCAATGTTGCTGTATGSCATTTGCACTGTGCTAGTGTGATGACCTATGACCTCATC 600
 Db 591 CCCAATGTTGCTGTATGSCATTTGCACTGTGCTAGTGTGATGACCTATGACCTCATC 650
 Qy 601 AAGATGCTCTCTGAAAGCCAACTGATGACATGACATGACCTCTGCACTTCACTTCT 660
 Db 651 AAGATGCTCTCTGAAAGCCAACTGATGACATGACATGACCTCTGCACTTCACTTCT 710
 Qy 661 GCC-TTGGGGGAGGCTTGTGACCACTGTCATGCGCTCC 700
 Db 711 GCCTTTGGGGAGGCTTGTGACCACTGTCATGCGCTCC 751

RESULT 8
 B1248501 927 bp mRNA linear EST 17-JUL-2001
 LOCUS 60292916F1 NCI_CGAP_Mams Mus musculus cDNA clone IMAGE:5148915 5',
 DEFINITION mRNA sequence.
 ACCESSION B1248501 GI:14794652
 VERSION B1248501.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 927)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-riemail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM11367 row: P column: 04
 High quality sequence stop: 919.
 Location/Qualifiers

FEATURES
 source 1..927
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:5148915"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /clone_1ib="NCI CGAP Mams"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt; site 2: NoCl; Cloned unidirectionally. Primer: Oligo dT. library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 180 a 296 c 248 g 203 t
 ORIGIN
 Query Match 72.3%; Score 672.8; DB 12; Length 927;
 Best Local Similarity 88.3%; Pred.No.1.5e-161;
 Matches 765; Conservative 0; Mismatches 97; Indels 4; Gaps 3;

Qy 61 GGCAAGCTGCTGTCATGCAATCTCATCACTTCTCTGATGATGCTAAAGTCGG 120
 Db 7 GTGCGAGCTGCTGTCATGCAATCTCATCACTTCTCTGATGATGCTAAAGTCGG 66
 Qy 121 TTACAGATCCAAAGAAAGTACGGGGCAGTCCGCTACAGCCAGCCAGTACCGC 180
 Db 67 CTGCAATCCAAAGGAGACTCAAGGCTAGTGGCACCGCAGCCAGTACCGT 126

Qy 181 GGTGTGATGGGACACATTCGACATGTGTGCTAGAGGAGCCCCGAAAGCCTCTACAT 240
 Db 127 GAGCTTCTGGATACATCTTAAACATAGTGTGACCTAGAGGTCCACCACTCTCAAT 186
 Qy 241 GGGCTGATGCGGAGCTTCAGCCGCAATAGACTTTGCTCTGTCCGATCGGCTGAT 300
 Db 187 GGGCTGATGCGGAGCTTCAGCCGCAATAGACTTTGCTCTGTCCGATCGGCTGAT 246
 Qy 301 GATTCTGTAAACAATTCTTACACCAAGGAGCTGTAGATGACATTTGGAGCGGCTC 360
 Db 247 GACTCTGTAAACAATTCTTACACCAAGGAGCTGTAGATGACATTTGGAGCGGCTC 306
 Qy 361 CTAGCAGCAGCAGCAGCAGTGCCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCT 420
 Db 307 CTGGCAGTACACCAAGTGCCTGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 366
 Qy 421 AAGTCCGATTCAGGCTCAGGCTGAGGCTGAGTGTGAGTACCAAGGAGCAGCTC 480
 Db 367 AAGTCCGATTCAGGCTCAGGCTGAGGCTGAGTGTGAGTACCAAGGAGCAGCTC 426
 Qy 481 AATGCTACAAAGCAATGCCCCAGAGAGAGGCTTCGGGAGCTCTGAGAAAGGACCTCT 540
 Db 427 GAGCTTACAAAGCAATGCCCCAGAGAGAGGCTTCGGGAGCTCTGAGAAAGGACCTCT 486
 Qy 541 CCCAATGTTGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
 Db 487 CCCAATGTTGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 Qy 600 CAAGATGCTCTCTGAAAGCCAACTGATGACATGACATGACATGACATGACATGAC 659
 Db 547 CAAGATGCTCTCTGAAAGCCAACTGATGACATGACATGACATGACATGACATGAC 606
 Qy 660 TGCCTTGGGGAGGCTTCTGCAACACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTG 719
 Db 607 TGCCTTGGGGAGGCTTCTGCAACACTGCTATGCTGCTGCTGCTGCTGCTGCTGCTG 666
 Qy 720 GAGTATCATGAATCTGCGCTGCGGAGTACAGTACAGTACAGTACAGTACAGTAC 779
 Db 667 GAGTATCATGAATCTGCGCTGCGGAGTACAGTACAGTACAGTACAGTACAGTAC 726
 Qy 780 GCTTCAGAGAGAGGAGGCTTCTGCAACACTGCTATGCTGCTGCTGCTGCTGCTGCT 839
 Db 727 GCTTCAGAGAGAGGAGGCTTCTGCAACACTGCTATGCTGCTGCTGCTGCTGCTGCT 786
 Qy 840 GGGTTCCTGGAAGTGTGATGTTGCTGCACTATGAGCAGTGAAGAGCCCTCATGCG 899
 Db 787 GGGTTCCTGGAAGTGTGATGTTGCTGCACTATGAGCAGTGAAGAGCCCTCATGCG 843
 Qy 900 TGCTTCGACTTCCGAGAGGCTGCTCT 925
 Db 844 TGCTTCGACTTCCGAGAGGCTGCTCT 869

RESULT 9
 AL542338 1201 bp mRNA linear EST 12-MAY-2003
 LOCUS AL542338 Homo sapiens PLACENTA Homo sapiens cDNA clone CS05D0107H17
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION AL542338
 VERSION AL542338.2 GI:30547386
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B.; Gruber, C.; Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12874284.
 Contact: Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3923.f. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D010CD090P2&cluster=3923.f. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D010CD090P2.

FEATURES

Location/Qualifiers

1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D010YH17"
 /issue_type="PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo (dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT

253 a 340 c 316 g 266 t 26 others

ORIGIN

Query Match

Best Local Similarity 92.3%; Pred. No. 2.2e-161; Indels 7; Gaps 5;
 Matches 736; Conservative 21; Mismatches 32;

1 ATGTTGGGTTCAAGGCGACAGATGTCGCTTCACTGCACTGTAAGTTCTTGGAGCT 60
 411 ATGTTGGGTTCAAGGCGACAGATGTCGCTTCACTGCACTGTAAGTTCTTGGAGCT 470
 61 GGCACAGCTGCTGATGCGAGATCTCATACCTTCTGATGTAAGTCCGG 120
 471 GGCACAGCTGCTGATGCGAGATCTCATACCTTCTGATGTAAGTCCGG 530
 121 TTACAGATTCAGAGGAGAAAGTCAGAGGCGCAGTGCCTACAGCGCCAGTACCG 180
 531 TTACAGATTCAGAGGAGAAAGTCAGAGGCGCAGTGCCTACAGCGCCAGTACCG 590
 181 GGTGATGAGGCGACCATTTCTGACATGATGCTGTAAGGCGCCGCAAGCTCTTCAAT 240
 591 GGTGATGAGGCGACCATTTCTGACATGATGCTGTAAGGCGCCGCAAGCTCTTCAAT 650
 241 GGGCTGTTGGCGGCTGACAGGCGCAATGAGCTTTCGCTGTCGCGATCGGCTGTAT 300
 651 GGGCTGTTGGCGGCTGACAGGCGCAATGAGCTTTCGCTGTCGCGATCGGCTGTAT 710
 301 GATTCTGTCAACAGATTCTTACACCAAGGGCTCTGAGCATGCGACATTGGAAGCCGCTC 360
 711 GATTCTGTCAACAGATTCTTACACCAAGGGCTCTGAGCATGCGACATTGGAAGCCGCTC 770
 361 CTAAGAGGAGAGACACAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 771 CTAAGAGGAGAGACACAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
 421 AAGTCCGATTCCAAAGCTCAGGCGCGGCTGAGTGTGAGAGATCAAAAGCACCGTC 480
 831 AAGTCCGATTCCAAAGCTCAGGCGCGGCTGAGTGTGAGAGATCAAAAGCACCGTC 890
 481 AATGCTTAACAACATTCGCGGAGAGAGAGGTTCCGGGGCTCTGAAAGGAGACCTCT 540
 891 AATGCTTAACAACATTCGCGGAGAGAGAGGTTCCGGGGCTCTGAAAGGAGACCTCT 950
 541 CCCAATGTTGCTGTAATGCGATTGTCACTGTGAGCT-GGTGACCTATGACCTCAT 599
 951 CCCAATGTTGCTGTAATGCGATTGTCACTGTGAGCTGAGGAGACCTATGACCTCAT 1010
 600 CAAAGATGCTCTCTGAAAGGCAACCTCATG-ACAGATGACCTCTCTGCACTTCACT 658
 1011 CAAAGATGCTCTCTGAAAGGCAACCTCATG-ACAGATGACCTCTCTGCACTTCACT 1070

659 CTCCTTTGGGAGGCTTCTGACCACTGTGATGCTCCCTCTGTAAAGCTGTCAAGA 718
 1071 CTCCTTTGGGAGGCTTCTGACCACTGTGATGCTCCCTCTGTAAAGCTGTCAAGA 1129
 719 CGAGATGATGAATCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 778
 1130 CG-GRDMMATGAATCTTGGCTTGGGSAK--ACATGAGAGCGCMCTKTCCTTCAAT 1185
 779 TGCTCCAGAGAGAGG 794
 1186 TSTACRAAGGGGGS 1201

RESULT 10
 AL581378/c 1201 bp mRNA linear EST 01-JUN-2003
 LOCUS
 DEFINITION
 AL581378 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
 clone CS0D005YK17-3-PRIME, mRNA sequence.
 AL581378
 VERSION
 KEYWORDS
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 On Feb 16, 2001 this sequence version replaced gi:12948318.
 Contact: Genoscope
 Genoscope - Centre National de Sequençage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5666.t. For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D005AF09NP1&cluster=5666.t. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0D005AF09NP1.

FEATURES

source

Location/Qualifiers

1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D005YK17"
 /issue_type="B CELLS (RAMOS CELL LINE)"
 /cell_line="RAMOS CELL LINE"
 /clone_id="Homo sapiens B CELLS (RAMOS CELL LINE)"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
 with a NotI-oligo (dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

BASE COUNT

282 a 250 c 377 g 207 t 85 others

ORIGIN

Query Match 70.9%; Score 659; DB 9; Length 1201;
 Best Local Similarity 97.6%; Pred. No. 5.9e-158;
 Matches 696; Conservative 11; Mismatches 2; Indels 4; Gaps 4;

219 GGGCCCCGGAAGCTCTACAAATGGCGTGTGCGGCTGCGGCGCAATGAGCTTGGC 278
 1073 VGGGCCCCGGAAGCTCTACAAATGGCGTGTGCGGCTGCGGCGCAATGAGCTTGGC 1016
 279 CTCGTGCGCATCGCGCTGTATGATTTGTCAACAGATTCTTACCAAGGCGCTTGAGCA 338
 1015 CTCGTGCGCATCGCGCTGTATGATTTGTCAACAG-TTACACCAAGGCGCTTGAGCA 957
 339 TGCCAGCATTTGGAGCGCGCTCTAGAGAG-CAGACCAAGAGTGCCTGCTGAGCGCTG 397


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Db      956 TGCCAGCATTTGGAGAGCGCTCTCTACAGAGCCAGAACACAGAGTCCCTGCTGGCTG 897
QY      398 TGAGCCAGCCAGCAGATGTGTGTAAGGTCCGATTCCAAAGCTAGAGCCCGGCTGAGAGTG 457
Db      896 TGAGCCAGCCAGCAGATGTGTGTAAGGTCCGATTCCAAAGCTAGAGCCCGGCTGAGAGTG 837
QY      458 GTGAGAGATACCAAGAGCCGATCATGCTTACAGAGCACTTCCGAGAGAGAGAGGTTCC 517
Db      836 GTGAGAGATACCAAGAGCCGATCATGCTTACAGAGCACTTCCGAGAGAGAGGTTCC 777
QY      518 GGGGCTCTGAGAAAGAGAGCTCTCCCAATGTGTCTGTAATCCATTTGCACTGTGCTG 577
Db      776 GGGGCTCTGAGAAAGAGAGCTCTCCCAATGTGTCTGTAATCCATTTGCACTGTGCTG 717
QY      578 AGCTGTGACCTTATGACCTCATAGAGATGCTCTGAAAGCCAAAGCTCATGACAGATG 637
Db      716 AGCTGTGACCTTATGACCTCATAGAGATGCTCTGAAAGCCAAAGCTCATGACAGATG 657
QY      638 ACCTCCCTGCACTTCACTTCTGCTTTGGGAGAGGCTTGTGCACTGTGATGCT 697
Db      656 ACCTCCCTGCACTTCACTTCTGCTTTGGGAGAGGCTTGTGCACTGTGATGCT 597
QY      698 CCCTGTGACCTGTGTCAAGAGATATGATGAACTGCTGAGGAGAGATGAGTACG 757
Db      596 CCCTGTGACCTGTGTCAAGAGATATGATGAACTGCTGAGGAGAGATGAGTACG 537
QY      758 CTGAGCACTGTGCTTATCCATGCTCCAGAGAGAGGAGCCGAGGCTTGTCAAGAGAGT 817
Db      536 CTGAGCACTGTGCTTATCCATGCTCCAGAGAGAGGAGCCGAGGCTTGTCAAGAGAGT 477
QY      818 TCATGCTCTCTTCTTCTGCTTGGGTTCTCGAAAGCTGTGATGTTCTGCACTTATGAGC 877
Db      476 TCATGCTCTCTTCTTCTGCTTGGGTTCTCGAAAGCTGTGATGTTCTGCACTTATGAGC 417
QY      878 AGCTGAACAGAGCCCTCATGCTGCTGACATTCCTGAGAGAGGCTCCCTTCTGA 930
Db      416 AGCTGAACAGAGCCCTCATGCTGCTGACATTCCTGAGAGAGGCTCCCTTCTGA 364

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RESULT 11
BI692548      938 bp      mRNA      linear      EST 18-SEP-2001
LOCUS      603343091.F1_NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5370646 5'
DEFINITION      mRNA sequence.
ACCESSION      BI692548
VERSION      BI692548.1 GI:15655177
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 938)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
TITLE      Unpublished
AUTHORS      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgapds-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1943 row: f column: 23
High quality sequence stop: 812.

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Source
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="PVB/N-3"
/db_xref="taxon:10090"

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/clone="IMAGE:5370646"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="MDH10B"
/clone_lib="NCI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: Salt;
Site 2: NCI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT      173 a      302 c      254 g      209 t
ORIGIN

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Query Match      70.2%; Score 652.4; DB 12; Length 938;
Best Local Similarity 88.1%; Freq. No. 2.5e-156;
Matches 721; Conservative 0; Mismatches 96; Indels 1; Gaps 1;

QY      109 GCTAAAGTCCGGTTACAGATCCAGAGAGAAAGTCAGAGGAGCCAGTGCAGCTACAGCCAGC 168
Db      2 GCTAAAGTCCGGTTACAGATCCAGAGAGAAAGTCAGAGGAGTAAAGGCTAAGTCCAGCCAGCCAGC 61
QY      169 GCCAGATACCGGCTGTATGAGGACCAATTCTGACATGTTGCTACTGAGGAGCCCGCA 228
Db      62 GCCAGATACCGGCTGTATGAGGACCAATTCTGACATGTTGCTACTGAGGAGTCAAGC 121
QY      229 AGCTCTCAATAGGCTGTGTTGCGGAGCTGAGAGCCAAATGAGCTTGTGCTGTGCTG 288
Db      122 AGCTCTCAATAGGCTGTGTTGCGGAGCTGAGAGCCAGATGAGCTTGTGCTGTGCTG 181
QY      289 ATCGGCTGTATGATTTCTGCAAAAGTTCTTACCAAGAGGCTGTGAGCATGCCAGATT 348
Db      182 ATCGGCTGTATGATTTCTGCAAAAGTTCTTACCAAGAGGCTGTGAGCATGCCAGATT 241
QY      349 GGGAGCGGCTCTGAGAGGAGACCAAGAGTGCCTGAGTGTGCTGAGCCCAAGC 408
Db      242 GGGAGCGGCTCTGAGAGTGCCTGAGTGCCTGAGTGTGCTGAGCCCAAGC 301
QY      409 ACGATGTGTAAAGTCCGATTCGACAGCTCAGGAGCCGAGCTGAGAGTGTGAGATAC 468
Db      302 ACGATGTGTAAAGTCCGATTCGACAGCTCAGGAGCCGAGCTGAGTGTGAGATAC 361
QY      469 CAAAGACCGCTCAATGCCCTACAGAGCCATGCCAGAGAGAGGAGTCCGAGGAGCTGTG 528
Db      362 CAAAGACCGCTCAATGCCCTACAGAGCCATGCCAGAGAGAGGAGTCCGAGGAGCTGTG 421
QY      529 AAAGGAGCTCTCCCAATGTTGCTGTATGCCATTGTCAACTGTGCTGAGCTGTGAC 588
Db      422 AAAGGAGCTCTCCCAATGTTGCTGTATGCCATTGTCAACTGTGCTGAGCTGTGAC 481
QY      589 TATGACCTCATAGATAGCCCTCCTGAAAGCCAACTGACAGATGACCTCCCTGC 648
Db      482 TATGACCTCATAGATAGCCCTCCTGAAAGCCAACTGACAGATGACCTCCCTGC 541
QY      649 CACTTCACTTGTGCTTGGGAGAGGCTTGTGACCACTGTGATGCTGCTGCTGTGAGC 708
Db      542 CACTTCACTTGTGCTTGGGAGAGGCTTGTGACCACTGTGATGCTGCTGCTGTGAGC 601
QY      709 GTGCTGAAGACAGATATCACTGCTGCTGAGGAGGCTGACAGTACAGGCTGAGCACTG 768
Db      602 GTGCTGAAGACAGATATCACTGCTGAGGAGGCTGACAGTACAGGCTGAGCACTG 661
QY      769 GCCCTTACCATGCTCCAGAGAGAGGAGCCGAGGCTTCTCAAGAGGTTGATGCCCTCC 828
Db      662 GCCCTTACCATGCTCCAGAGAGAGGAGCCGAGGCTTCTCAAGAGGTTGATGCCCTCC 721
QY      829 TTTCTCGCTTGGGTTCTCTGGAAGTGTGATGTTCTGACCTATGAGCACTGAAGAGA 888
Db      722 TTTCTCGCTTGGGTTCTCTGGAAGTGTGATGTTCTGACCTATGAGCACTGAAGAGA 780
QY      889 GCCCTATGAGCTGCTGCACTTCCGAGAGGCTCCCTT 926
Db      781 CCTTATGAGGCTGCTACCAATCTGGGAGAGGCACTT 818

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RESULT 12
AL575087/c 1125 bp mRNA linear EST 01-JUN-2003
LOCUS
DEFINITION AL575087 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD10631E20 3-PRIME, mRNA sequence.
ACCESSION
AL575087
VERSION
AL575087.2 GI:31313395
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1125)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
On Feb 16, 2001 this sequence version replaced gi:12935911.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5666.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOD10631E20&cluster=5666.r Contact :
Peng Liang Email: filiang@life.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD10631E20.
FEATURES
source
1..1125
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD10631E20"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 264 a 252 c 349 g 207 t 53 others
ORIGIN
Query Match 69.6% Score 647.6; DB 9; Length 1125;
Best Local Similarity 93.3% Pred. No. 4.8e-155;
Matches 667; Conservative 25; Mismatches 20; Indels 3; Gaps 2;
QY 219 GGGCCCCGGAAGCTCTCAATGGGCTGTTGGCGGCTGAGGCGCAATGAGCTTGC 278
DB 1028 GGGSCCCCGAAGCTCTTACATGGGCTGCGCGGCTTGAGCGCAATGAGCTTGC 969
QY 279 CTCTGCGCGCATCGGCTGTATGATTTGTCAACAGTTCTACACAGGCTCTGAGCA 338
DB 968 YCTCTCCGCAATCGCTGTATGATTTGTCAACAGTTCTACACAGGCTCTGAGCA 909
QY 339 TCCAGCATTTGGGAAGCGGCTCTCTAGCAGGAGCAACACAGTGCCTGCTGTGCTGT 398
DB 908 TCCAGCATTTGGGAAGCGGCTCTCTAGCAGGAGCAACACAGTGCCTGCTGTGCTGT 849
QY 399 GGGCCAGCCCAAGGATGGTAAAGTCCGATTCAGCTCAGGCGCGGCTGAGAGTGG 458
DB 848 GGGCCAGCCCAAGGATGGTAAAGTCCGATTCAGCTCAGGCGCGGCTGAGAGTGG 789
QY 459 TCGAGATACCAAGACCGTCAATGCTTACAGACCAATGCTCCGAGAGAGAGGTTCCG 518
DB 788 TCGAGATACCAAGACCGTCAATGCTTACAGACCAATGCTCCGAGAGAGAGGTTCCG 729
QY 519 GGGCTCTGGAAGAGGAGCTCTCCCAATGTTGCTGTATGCTGCACTGCTGCTGA 578
DB 728 GGGCTCTGGAAGAGGAGCTCTCCCAATGTTGCTGTATGCTGCACTGCTGCTGA 669
QY 579 GCTGTGACTATGACTCATCAGATGAGTCCCTCTGAAAGCAACTCATGACATGA 638

Db 668 GCTGAGACCTATGACCTCATCAGAGGCTCTGTAAGGCAACCTCATGACATGA 609
QY 639 CTCTCCCTGCACTTCACTTCTGCTTTGGGAGGCTTCTGCA--CCAGTCAATGCC 696
Db 608 CTCTCCCTGCACTTCACTTCTGCTTTGGGAGGCTTCTGCAACATGATCATGCC 549
QY 697 TCCCTGTGAGCTGTCAAGCAGATACATCACTCTGCGCTGGGCACTAGAGTGC 756
Db 548 TCCCTGTGAGCTGTCAAGCAGATACATCACTCTGCGCTGGGCACTAGAGTGC 489
QY 757 GCTGAGACCTGCTCTTCACTGCTCCAGAGAGGAGGCGGCTTCTGCAAGAGG 816
Db 488 GCTGAGACCTGCTCTTCACTGCTCCAGAGAGGAGGCGGCTTCTGCAAGAGG 429
QY 817 TCCATGCTCTCTTCTGCTGCTTTGGGCTTCTGCAAGCTGTATGTTGTCACCTATAG 876
Db 428 TCCATGCTCTCTTCTGCTGCTTTGGGCTTCTGCAAGCTGTATGTTGTCACCTATAG 369
QY 877 CAGCTGAAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 930
Db 368 CAGCTGAAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 314
RESULT 13
BF976529 859 bp mRNA linear EST 22-JAN-2001
LOCUS
DEFINITION BF976529 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:433533 5',
mRNA sequence.
ACCESSION
BF976529
VERSION
BF976529.1 GI:12343744
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 859)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: rgabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1206 row: d column: 22
High quality sequence stop: 807.
FEATURES
source
1..859
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:433533"
/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 144 a 276 c 223 g 216 t
ORIGIN
Query Match 68.9% Score 640.6; DB 10; Length 859;

Fri Feb 6 16:59:29 2004

us-09-884-814-2.rst

Page 13

[illegible]

QY	181	GGGTGTGATGGGACACATTCTGACCAATGATGCTGACTGAGAGGACCCCGAAGCTCTACAAAT	240
Db	544	GGTGTGATGGGACCAATTCTGACCAATGATGCTGACTGAGAGGACCCCGAAGCTCTACAAAT	603
QY	241	GGGCTGTGTGCGCGGCTGTGACAGCGCAATGAGCTTGGCTCTGTGTCGGATGCGGCTGTAT	300
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QY	301	GATTCTGTCAAAACAGTTCTACACCAAGAGGCTCTGAGCATGCGAGCAATGGAGCGGCTCT	360
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QY	361	CTAGCAGGCAAGACCAACAGGTGCGCTGATGCTGTGATGAGCCAGCCAGCAATGTGGTA	420
Db	724	CTAGCAGGCAAGACCAACAGGTGCGCTGATGCTGTGATGAGCCAGCCAGCAATGTGGTA	783
QY	421	AAGGTCGCAATTCAGAGCTCAAGGCCCGGCTGAGAGGTGTGTGAGATATCCAAAGCACCGTC	480
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QY	481	AATGCTCTACAAACCATTTGCCCCGAGAGAAAGGTTCCGGGACCTCTGAAAAGGACCTCT	540
Db	844	AATGCTCTACAAACCATTTGCCCCGAGAGAAAGGTTCCGGGACCTCTGAAAAGGACCTCT	903
QY	541	CCCAATGTTGCTCGTATGATGCCATTGTCAACTGTGTCTGAGGTGTGTGACTATACCTCAATC	600
Db	904	CCCAATGTTGCTCGTATGATGCCATTGTATATGATGTGTGACTATACCTCAATC	963
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QY	661	GCGTTTGGGAGAGCTTGTGACCACTGTCAATGCGCTCCCTGTAGACGTGTCAAAGAC	720
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QY	721	A 721	
Db	1081	A 1081	

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Search completed: February 4, 2004, 20:08:11
Job time : 2418 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:15:38 ; Search time 42 Seconds

(without alignments)
1167.774 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576

Sequence: 1 MWGFADVPPTATVKTGA.....TYEQLKALMAACTSREAPP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 156726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1576	100.0	309	AA1903	Human uncoupling p
2	1576	100.0	309	AA28351	UCP2 amino acid se
3	1576	100.0	309	AA45002	Tularik human unco
4	1576	100.0	309	AA45292	Human uncoupling p
5	1576	100.0	309	AA72342	Human uncoupling p
6	1576	100.0	314	AA109077	Human uncoupling p
7	1576	99.7	309	AAW24000	Complete chimeric
8	1572	99.7	309	AA28353	UCP2 amino acid se
9	1572	99.7	309	AAW89546	Full length human

10	1572	99.7	309	AA27018	Protein associated
11	1572	99.7	309	AA197998	Human uncoupling p
12	1572	99.7	309	AA44252	Human mitochondria
13	1570	99.6	309	AAW69166	Human respiration
14	1570	99.6	309	AA28352	UCP2 amino acid se
15	1570	99.6	309	AA198901	Human uncoupling p
16	1565	99.3	309	AAW85669	Human UCP-2 (uncou
17	1551	98.4	305	AA191282	Body weight disord
18	1520	96.4	299	AAW23988	Partial human C5 g
19	1520	95.1	299	AA191281	Human body weight
20	1499	95.1	299	AAW23987	Human C5 gene prod
21	1282	81.3	303	AA197997	Mouse uncoupling p
22	1279	81.2	303	AAW89545	Full length mouse
23	1279	81.2	303	AAW89545	Protein associated
24	1273	80.8	303	AA191280	Brown fat uncoupli
25	1181.5	75.0	397	AAW81586	Protein encoded by
26	1180.5	74.9	308	AAW81585	Mouse uncoupling p
27	1180.5	74.9	308	AAW8280	Mouse uncoupling p
28	1178.5	74.8	308	AA192834	Mouse uncoupling p
29	1178.5	74.8	308	AAW85116	Murine uncoupling
30	1178.5	74.8	308	AA197452	Murine mitochondri
31	1178.5	74.8	308	AA197452	Mouse uncoupling p
32	1162.5	73.8	432	AA192835	Mouse uncoupling p
33	1162.5	73.8	432	AAW85117	A murine uncouplin
34	1162.5	73.8	432	AA197453	Murine mitochondri
35	1162.5	73.8	432	AA197453	Mouse uncoupling p
36	1149.5	72.9	312	AAW83379	Human uncoupling p
37	1149.5	72.9	312	AAW8197	Human uncoupling p
38	1149.5	72.9	312	AA191904	Human UCP-3 (uncou
39	1149.5	72.9	312	AAW85657	Human uncoupling p
40	1149.5	72.9	312	AAW8279	Human uncoupling p
41	1149.5	72.9	312	AA194600	Amino acid sequenc
42	1149.5	72.9	312	AA194600	Human mitochondria
43	1149.5	72.9	312	AA194600	Human uncoupling p
44	1149.5	72.9	312	AAE04258	Amino acid sequenc
45	1149.5	72.9	312	AAW8050	Human UCP3 protein

ALIGNMENTS

RESULT 1	AA191903	
ID	AA191903	standard; Protein; 309 AA.
XX	AA191903;	
AC	21-DEC-1999	(first entry)
XX		
DT	Human uncoupling protein 2.	
XX		
DE	Human uncoupling protein 2.	
XX		
KW	Uncoupling protein 2; UCP2; human; obesity; diabetes; diagnosis;	
KM	gene therapy.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference	SS
FT	/note=	"this residue is substituted by Val in variant"
XX		
XX	MO948905-A1.	
XX		
PD	30-SEP-1999.	
XX		
XX	23-MAR-1999;	99MO-US06317.
XX		
XX	23-MAR-1998;	98US-0078972.
PR		
XX	(MUSC-) MUSC FOUND RES DEV.	
PA		
XX		
XX	Garvey WT, Argypoulos G;	
PI		

DR WPI; 1999-591072/50.
 DR N-PSDB; AAZ19967, AAZ19968.
 XX
 XX Use of uncoupling protein 2 or 3 as markers for identifying subjects
 PT at risk of developing obesity or diabetes -
 XX
 XX
 PS Claim 9; Page 102; 112pp; English.
 CC The present sequence represents human uncoupling protein 2 (UCP2).
 CC The invention relates to the discovery that the presence of
 CC single nucleotide polymorphisms, such as C164T in the UCP2 gene (see
 CC AAI9967 and AAI9968), correlate with the development of obesity
 CC and/or type II diabetes mellitus. This polymorphism results in
 CC substitution of valine for alanine at amino acid position 55 of the
 CC present sequence. Methods are provided for identifying a subject
 CC at risk of developing obesity and/or diabetes by detection of the
 CC polymorphism in the UCP2 nucleic acid or amino acid sequence. An
 CC antibody to an antigen of the altered UCP2 can be used in such a
 CC method. 3 Further polymorphisms, in UCP3 (see AAY1903), are also
 CC correlated with obesity and diabetes.
 CC
 XX
 SQ Sequence 309 AA;
 Query Match 100.0%; Score 1576; DB 20; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-158;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGRATDVPPATVVKFLGAGTACIADLITPFLDTAKVRLQIGSSGQPVATASQYR 60
 DB 1 MVGRATDVPPATVVKFLGAGTACIADLITPFLDTAKVRLQIGSSGQPVATASQYR 60
 QY 61 GVGGITLMTWRETPRSILYNGLVAGLQROMSPASVRIGLYDSVKQFYTGSEHASIGSRL 120
 DB 61 GVGGITLMTWRETPRSILYNGLVAGLQROMSPASVRIGLYDSVKQFYTGSEHASIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAQAAGGGRVOSTVNAKTIAREBGRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAQAAGGGRVOSTVNAKTIAREBGRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVTYDILIKDALLKANIMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
 DB 181 PNVARNAIVNCAELVTYDILIKDALLKANIMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYMNSALGQYSSAGHCALITMLQKEGPRAFYKGFMSFLRLGSMNVVMFTYEQLRALMA 300
 DB 241 RYMNSALGQYSSAGHCALITMLQKEGPRAFYKGFMSFLRLGSMNVVMFTYEQLRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 Db 301 ACTSREAPF 309
 RESULT 2
 ID AAY28351
 XX AAY28351 standard; protein; 309 AA.
 AC AAY28351;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE UCP2 amino acid sequence.
 XX
 KW uncoupling protein; amino acid; mitochondria; diabetes;
 KW brown adipose tissue; wild type; obesity; thermo-regulation.
 XX
 OS Homo sapiens.
 XX
 PN WO9337812-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1999; 99WO-US01198.
 XX

PR 23-JAN-1998; 98US-0012218.
 XX
 PA (ORCH-) ORCHID BIOCOMPUTER INC.
 XX
 PI Vrolijk LP;
 XX
 DR WPI; 1999-469144/35.
 DR N-PSDB; AAX9434.
 XX
 XX A novel single nucleotide polymorphism of the uncoupling protein 2
 PT gene, useful for diagnosis, prognosis and treatment of obesity
 PS Disclosure; Fig 1; 68pp; English.
 CC This is the amino acid sequence of uncoupling protein-2 (UCP-2) as
 CC reported by Boss et al, FEBS Lett. 408, 39-42 1997.
 CC Identifying a UCP2 polymorphism, especially Val55 (thymine at
 CC nucleotide 164), can be used to diagnose obesity, non-insulin dependent
 CC diabetes mellitus and other UCP2 related diseases. Wild-type UCP2
 CC generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2
 CC related diseases include atherosclerosis, hyperinsulinemia, chronic
 CC inflammation, thermogenesis, apoptosis and cachexia.
 CC
 XX
 SQ Sequence 309 AA;
 Query Match 100.0%; Score 1576; DB 20; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-158;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGRATDVPPATVVKFLGAGTACIADLITPFLDTAKVRLQIGSSGQPVATASQYR 60
 DB 1 MVGRATDVPPATVVKFLGAGTACIADLITPFLDTAKVRLQIGSSGQPVATASQYR 60
 QY 61 GVGGITLMTWRETPRSILYNGLVAGLQROMSPASVRIGLYDSVKQFYTGSEHASIGSRL 120
 DB 61 GVGGITLMTWRETPRSILYNGLVAGLQROMSPASVRIGLYDSVKQFYTGSEHASIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAQAAGGGRVOSTVNAKTIAREBGRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAQAAGGGRVOSTVNAKTIAREBGRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVTYDILIKDALLKANIMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
 DB 181 PNVARNAIVNCAELVTYDILIKDALLKANIMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYMNSALGQYSSAGHCALITMLQKEGPRAFYKGFMSFLRLGSMNVVMFTYEQLRALMA 300
 DB 241 RYMNSALGQYSSAGHCALITMLQKEGPRAFYKGFMSFLRLGSMNVVMFTYEQLRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 Db 301 ACTSREAPF 309
 RESULT 3
 ID AAY45002
 XX AAY45002 standard; Protein; 309 AA.
 AC AAY45002;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Tularik human uncoupling protein-2.
 XX
 KW Human uncoupling protein-2; UCP2; body weight disorder; screening assay;
 KW obesity; underweight disorder; anorectic; anabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200006087-A2.
 XX
 PD 10-FEB-2000.
 XX

DT 24-APR-2001 (first entry)
 XX Human uncoupling protein, UCP-2.
 XX
 DE Human uncoupling protein, UCP-2.
 XX
 XX Human; uncoupling protein; UCP-2; cancer; brain; renal; antiviral;
 KM antibacterial; antifungal; cytostatic; immunosuppressive; scleroderma;
 KM antiarthritic; dermatological; UCP inhibitor; therapy; antithematic;
 KM rheumatoid arthritis; leukaemia; tumour; autoimmune disease; SLE;
 KM systemic lupus erythematosus; celiac disease; infectious disease;
 KM pemphigus vulgaris.
 XX
 OS Homo sapiens.
 XX
 PN W0200078941-A2.
 XX
 PD 28-DEC-2000.
 XX
 XX 22-JUN-2000; 2000WC-US17245.
 XX
 XX 23-JUN-1999; 99US-0140574.
 PR
 PA (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
 XX
 PI Newell MK;
 XX
 XX WPI; 2001-102716/11.
 DR N-PSDB; AAD02388.
 DR
 XX Inhibiting plasma membrane uncoupling protein expression in tumor cells
 PT and rapidly dividing bacterial cells, for treating cancer and
 PT infectious diseases -
 PT
 PS Disclosure; Page 104-105; 106pp; English.
 XX
 XX The present sequence is human uncoupling protein, UCP-2. The
 CC present invention relates to a method for inhibiting the expression
 CC of plasma membrane uncoupling protein (UCP) in a cell by a plasma
 CC membrane UCP inhibitor. UCP is expressed on lysosomal membranes
 CC and plasma membranes of rapidly dividing cells, but absent in growth
 CC arrested or chemotherapy resistant cells. This method is useful in the
 CC inhibition of plasma membrane UCP expression in tumor cells,
 CC lymphocytes, pancreatic beta cells, rapidly dividing bacterial cells
 CC or B cells. UCP inhibitor is useful in the prevention and treatment of
 CC infectious disease, rheumatoid arthritis, scleroderma and cancers such
 CC as brain cancer, leukemia, renal cancer, and tumours. The UCP activator
 CC is useful in the treatment of autoimmune diseases such as systemic
 CC lupus erythematosus (SLE), celiac disease and pemphigus vulgaris. UCP
 CC is also useful for inducing cellular division in nerve cells.
 XX
 XX Sequence 309 AA;
 SQ
 Query Match 100.0%; Score 1576; DB 22; Length 309;
 Best Local Similarity 100.0%; Pred. No. 3.1e-158;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGFKATDVPPATATVFLGAGTAACTADITPPLDTAKVRLQIGESOGPVATASQYR 60
 DB 1 MVGFKATDVPPATATVFLGAGTAACTADITPPLDTAKVRLQIGESOGPVATASQYR 60
 QY 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLDSVKQFYTKGSHASIGSRL 120
 DB 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLDSVKQFYTKGSHASIGSRL 120
 QY 121 LAGSTTGALAAVAAPPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREEGFGMLKGT 180
 DB 121 LAGSTTGALAAVAAPPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREEGFGMLKGT 180
 QY 121 LAGSTTGALAAVAAPPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREEGFGMLKGT 180
 DB 121 LAGSTTGALAAVAAPPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREEGFGMLKGT 180
 QY 181 PVARNALVNCHELTVDLIDALLKAVLMTDDI.PCHFTSAFGAGCTTYIASPVDVVKI 240
 DB 181 PVARNALVNCHELTVDLIDALLKAVLMTDDI.PCHFTSAFGAGCTTYIASPVDVVKI 240
 QY 241 RYMNSALGOYSSAGHCALTMLQKSGPRAFYKGFVPSFLRIGSNVNVFVITYEOLKRALMA 300
 DB 241 RYMNSALGOYSSAGHCALTMLQKSGPRAFYKGFVPSFLRIGSNVNVFVITYEOLKRALMA 300

DB 241 RYMNSALGOYSSAGHCALTMLQKSGPRAFYKGFVPSFLRIGSNVNVFVITYEOLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 RESULT 6
 AAU09077
 ID AAU09077 standard; Protein, 314 AA.
 XX
 AC AAU09077;
 XX
 XX 13-DEC-2001 (first entry)
 DT
 XX Human uncoupling protein, UCP-2.
 DE
 XX Human; uncoupling protein; UCP-2; transgenic plant; fuel metabolism;
 KM antibacterial; bacterial infection; environmental stress; food.
 KM
 XX Homo sapiens.
 OS
 PN W0200175131-A2.
 XX
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WC-US10236.
 PF
 XX 31-MAR-2000; 2000US-193533P.
 PR
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 XX Berry-Lowe SL, Newell MK;
 PI
 XX WPI; 2001-626442/72.
 DR N-PSDB; AAS14819.
 DR
 XX Plants expressing heterologous cell-wall uncoupling protein, have
 PT altered metabolism, resistance to infection and stress sensitivity -
 PT
 PS Disclosure; Page 59-60; 72pp; English.
 XX
 XX The invention relates to a transgenic plant expressing a cell-wall UCP
 CC (uncoupling protein) encoded by a heterologous gene. The
 CC heterologous UCP, when expressed in the plant cell wall, plasma
 CC membrane or chloroplast regulates the fuel metabolism of the plant.
 CC Regulating expression or activity of UCP is used to control fuel
 CC metabolism, especially reducing UCP expression produces nutritionally
 CC improved plants and protects against infection e.g. bacterial, while
 CC decreasing expression improves sensitivity to light and cold. Altering
 CC UCP activity can improve crop productivity and durability towards
 CC environmental stress, and it eliminates time-consuming and expensive
 CC maintenance and repeated application of chemicals. The present
 CC sequence represents human UCP-2 and is used as the heterologous UCP in
 CC the method of the invention.
 XX
 XX Sequence 314 AA;
 SQ
 Query Match 100.0%; Score 1576; DB 22; Length 314;
 Best Local Similarity 100.0%; Pred. No. 3.2e-158;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVGFKATDVPPATATVFLGAGTAACTADITPPLDTAKVRLQIGESOGPVATASQYR 60
 DB 6 MVGFKATDVPPATATVFLGAGTAACTADITPPLDTAKVRLQIGESOGPVATASQYR 65
 QY 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLDSVKQFYTKGSHASIGSRL 120
 DB 61 GVMGTLTMTWRTGPRSLVNGLVAGLORQMSFASVRIGLDSVKQFYTKGSHASIGSRL 125
 QY 121 LAGSTTGALAAVAAPPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREEGFGMLKGT 180
 DB 121 LAGSTTGALAAVAAPPTDVVKVRFQAQARAGGRRYOSTVNAVYKTIAREEGFGMLKGT 185

QY 181 PNVARNAIIVNCAELVYDILKDALIKANIMTDLPCHFTSAFGAGFCTTVIASPVVYKT 240
 DB 186 PNVARNAIIVNCAELVYDILKDALIKANIMTDLPCHFTSAFGAGFCTTVIASPVVYKT 245
 QY 241 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMVTEYEQKRALMA 300
 DB 246 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMVTEYEQKRALMA 305
 QY 301 ACTSREAPF 309
 DB 306 ACTSREAPF 314

RESULT 7
 AAM24000
 ID AAM24000 standard; Protein; 309 AA.

AC AAM24000;
 DT 28-MAY-1998 (first entry)
 DE Complete chimeric mouse/human C5 gene product.
 KW Human; mouse; C5 gene; weight disorder; obesity; chimeric.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 XX US5702902-A.
 XX 30-DEC-1997.
 PE 23-AUG-1995; 95US-0518878.
 ER 23-AUG-1995; 95US-0518878.
 PR 23-AUG-1994; 94US-0294522.
 PR 06-JUN-1995; 95US-0470868.
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Tartaglia LA;
 DR WPI; 1999-076410/07.
 XX
 PT Diagnosis of body weight disorders - by detecting abnormal C5 gene expression
 PS Claim 1; Column 87-88; 71pp; English.
 CC This is the amino acid sequence for the chimeric murine/human C5 protein.
 CC The C5 gene shows differential expression in body weight disorder states
 CC relative to expression in a normal body. Body weight disorders can be
 CC diagnosed using tests comprising the detection of abnormal levels of
 CC the C5 gene transcript (or the encoded protein). The method can be used
 CC to diagnose, e.g. obesity.
 XX Sequence 309 AA;

Query Match 99.7%; Score 1572; DB 19; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVEFKATDVPPTATVVFELAGTACTADITPPLDTAKVRLIOGESGQPVRAVSAQYR 60
 DB 1 MVEFKATDVPPTATVVFELAGTACTADITPPLDTAKVRLIOGESGQPVRAVSAQYR 60
 QY 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDVKQFYTKGSEHASISGRL 120
 DB 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDVKQFYTKGSEHASISGRL 120
 QY 121 LAGSTGALAAVAAQPTDVVKVRFQQAARAGGRRYQSTVNAKYTIAEEGFRGLMKGTS 180
 DB 121 LAGSTGALAAVAAQPTDVVKVRFQQAARAGGRRYQSTVNAKYTIAEEGFRGLMKGTS 180

DB 121 LAGSTGALAAVAAQPTDVVKVRFQQAARAGGRRYQSTVNAKYTIAEEGFRGLMKGTS 180
 QY 181 PNVARNAIIVNCAELVYDILKDALIKANIMTDLPCHFTSAFGAGFCTTVIASPVVYKT 240
 DB 186 PNVARNAIIVNCAELVYDILKDALIKANIMTDLPCHFTSAFGAGFCTTVIASPVVYKT 245
 QY 241 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMVTEYEQKRALMA 300
 DB 246 RYNSALGOYSSAGHCLTWTLOKEGPRAFYKGFMSFRLGSMNVVMVTEYEQKRALMA 305
 QY 301 ACTSREAPF 309
 DB 306 ACTSREAPF 314

RESULT 8
 AAY28353
 ID AAY28353 standard; Protein; 309 AA.

AC AAY28353;
 DT 19-OCT-1999 (first entry)
 DE UCP2 amino acid sequence (Glimmo variant).
 KW uncoupling protein; amino acid; mitochondria; diabetes;
 KW brown adipose tissue; wild type; obesity; thermo-regulation.
 OS Homo sapiens.
 XX WO9937812-A1.
 XX 29-JUL-1999.
 PE 21-JAN-1999; 99WO-US01198.
 PR 23-JAN-1998; 98US-0012218.
 PA (ORCH-) ORCHID BIOCOMPUTER INC.
 PI Vrolijk LP;
 DR WPI; 1999-468144/39.
 DR N-PEDB; AAX99436.
 XX
 PT A novel single nucleotide polymorphism of the uncoupling protein 2
 PT gene, useful for diagnosis, prognosis and treatment of obesity
 PS Disclosure; Fig 1; 68pp; English.
 CC This is the amino acid sequence of uncoupling protein-2 (UCP-2) as
 CC reported by Glimmo et al, 1997 (direct submission).
 CC Identifying a UCP2 polymorphism, especially Val55 (thymine at
 CC nucleotide 164), can be used to diagnose obesity, non-insulin dependent
 CC diabetes mellitus and other UCP2 related diseases (claimed). Wild-type
 CC UCP2 generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2
 CC related diseases include atherosclerosis, hyperinsulinemia, chronic
 CC inflammation, thermogenesis, apoptosis and cachexia.
 XX Sequence 309 AA;

Query Match 99.7%; Score 1572; DB 20; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVEFKATDVPPTATVVFELAGTACTADITPPLDTAKVRLIOGESGQPVRAVSAQYR 60
 DB 1 MVEFKATDVPPTATVVFELAGTACTADITPPLDTAKVRLIOGESGQPVRAVSAQYR 60
 QY 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDVKQFYTKGSEHASISGRL 120
 DB 61 GVMGTITLWRTGPRSLYNGVLVAGLQROMSPASVRIGLYDVKQFYTKGSEHASISGRL 120

QY 121 LAGSTGALAVAAQPTDVVKRFQAGAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 DB 121 LAGSTGALAVAAQPTDVVKRFQAGAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVYDILKDALLKANIMTDLPCHFTSAFGAGCTTVIASPDVYKT 240
 DB 181 PNVARNAIVNCAELVYDILKDALLKANIMTDLPCHFTSAFGAGCTTVIASPDVYKT 240
 QY 241 RYMSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 9
 ID AAM89546 standard; Protein; 309 AA.
 AC AAM89546;
 XX
 DT 31-MAR-1999 (first entry)
 XX
 DE Full length human C5 protein sequence.
 XX
 KW Body weight disorder; obesity; appetite regulation; thermoregulation;
 XX anorexia; abnormal food intake; cachexia; thermogenesis.
 OS Homo sapiens.
 PN US5853975-A.
 XX
 PD 29-DEC-1998.
 XX
 PF 26-FEB-1997; 97US-0807861.
 XX
 PR 26-FEB-1997; 97US-0807861.
 PR 23-AUG-1994; 94US-0294522.
 PR 06-JUN-1995; 95US-0470868.
 PR 23-AUG-1995; 95US-0518878.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Tartaglia LA;
 XX
 DR MPI: 1999-054892/08.
 DR N-PSDB; AAV82381.
 XX
 PT Identifying modulators of C5 protein uncoupling activity - used as
 XX potential regulators of thermogenesis, appetite and body weight,
 XX e.g. for treating obesity, anorexia and cachexia
 PS Claim 7; Fig 16; 83pp; English.

The present invention describes a method for identifying a compound (I) that modulates C5 protein uncoupling activity by: (a) treating a test compound with C5 or cells expressing it; (b) measuring the level of uncoupling activity; and (c) comparing this with level of activity in the absence of the test compound. Any difference in the levels indicates a modulator. C5 protein has uncoupling activity, i.e. it can transport protons across the mitochondrial inner membrane, reducing the proton motive force and allowing dissipation of caloric energy as heat. It is thus a regulator of thermogenesis and is involved in body weight regulation. (I) are potentially useful in treatment of body weight disorders, regulation of appetite and thermoregulation, e.g. in cases of obesity, anorexia, abnormal food intake and cachexia. The present sequence represents the full length human C5 protein sequence, from the present invention.

Query Match 99.7%; Score 1572; DB 20; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPNATVYFIFGAGFAACTADLPEDTAKVRLQIGESGQPYRATASQYR 60
 DB 1 MVGFKATDVPPNATVYFIFGAGFAACTADLPEDTAKVRLQIGESGQPYRATASQYR 60
 QY 61 GWGKTLITWREGEPSLYNGLVAGLQRMSPASVRIQLYDSVKQFYTKGSEHASISRL 120
 DB 61 GWGKTLITWREGEPSLYNGLVAGLQRMSPASVRIQLYDSVKQFYTKGSEHASISRL 120
 QY 121 LAGSTGALAVAAQPTDVVKRFQAGAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 DB 121 LAGSTGALAVAAQPTDVVKRFQAGAGGRRYQSTVNAKTIAREEGRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVYDILKDALLKANIMTDLPCHFTSAFGAGCTTVIASPDVYKT 240
 DB 181 PNVARNAIVNCAELVYDILKDALLKANIMTDLPCHFTSAFGAGCTTVIASPDVYKT 240
 QY 241 RYMSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMSALGQYSSAGHCALTMLQKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 10
 ID AAB27018 standard; Protein; 309 AA.
 AC AAB27018;
 XX
 DT 06-FEB-2001 (first entry)
 XX
 DE Protein associated with body weight disorders, SEQ ID NO: 51.
 XX
 KW Mouse; body weight; immunomodulator; anorectic; obesity; cachexia;
 XX thermogenesis; appetite.
 OS Mus sp.
 PN US6121017-A.
 XX
 PD 19-SEP-2000.
 XX
 PF 08-OCT-1997; 97US-0946719.
 XX
 PR 26-FEB-1997; 97US-0807861.
 PR 23-AUG-1994; 94US-0294522.
 PR 06-JUN-1995; 95US-0470868.
 PR 23-AUG-1995; 95US-0518878.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Tartaglia LA;
 XX
 DR MPI: 2000-618197/59.
 DR N-PSDB; AAA99716.
 XX
 PT New human C5 gene and gene product, useful in regulating mammalian body
 XX weight and modulating thermogenesis, especially useful for treating
 XX body weight disorders, e.g. obesity or cachexia
 PS Claim 1; Fig 17B; 84pp; English.

The present sequence is encoded by a nucleotide sequence which was found to be differentially expressed in body weight disorder states. It may be useful in modulating processes relating to mammalian body weight regulation, including treatment of body weight disorders, e.g. obesity or cachexia, and modulation of thermogenesis. It is also

CC useful in regulating appetite and/or body weight. Furthermore, it is
 CC useful for diagnostic evaluation and prognosis of various body weight
 CC disorders, and for identifying subjects exhibiting a predisposition to
 CC such conditions.

XX Sequence 309 AA;

Query Match 99.7%; Score 1572; DB 21; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8,2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPTATVFKFLGAGTAACTADLTLPDLTAKVRLQIQESQGPVRAVTAQAQR 60
 DB 1 MVGFKATDVPPTATVFKFLGAGTAACTADLTLPDLTAKVRLQIQESQGPVRAVTAQAQR 60
 QY 61 GVGTTILMTVRTGPRSLYNGLVAGLQROMSPASVRIGLDSVKQFTYKSGEHSIGSRL 120
 DB 61 GVGTTILMTVRTGPRSLYNGLVAGLQROMSPASVRIGLDSVKQFTYKSGEHSIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAQAPAGGRRYOSTVNAVYKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAQAPAGGRRYOSTVNAVYKTIAREEGFRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVTYDLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 DB 181 PNVARNAIVNCAELVTYDLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 QY 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVMEVTEQLKRALMA 300
 DB 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVMEVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 11
 ID AAY97998 standard; Protein; 309 AA.

XX AAY97998;
 XX 18-SEP-2000 (first entry)

DE Human uncoupling protein C5, SEQ ID NO:51.

XX Body weight disorder; obesity; cachexia; differential expression;
 KW human; C5 gene; C5 protein; UCP homologue; uncoupling protein;
 KM thermogenesis; expression modulation.

XX Homo sapiens.

OS Homo sapiens.

XX US6057109-A.

XX US6057109-A.

XX 02-MAY-2000.

XX 14-DEC-1998; 98US-0210681.

XX 26-FEB-1997; 97US-0807861.

XX 08-OCT-1997; 97US-0946719.

XX 23-AUG-1994; 94US-0294522.

XX 06-JUN-1995; 95US-0470868.

XX 23-AUG-1995; 95US-0518878.

XX (MILL-) MILLENNIUM PHARM INC.

XX Tartaglia LA;

XX WPI; 2000-338601/29.

XX N-PSDB; AAA52254.

XX Identifying C5 gene expression modulators useful for treating obesity
 PT and cachexia comprises comparing levels of C5 expression prior to or

PT after contacting it with test compound -
 XX Examples; Fig 18A-B; 84pp; English.

XX The invention relates to a method for identifying a compound that
 CC modulates expression of the novel gene C5. The method comprises
 CC contacting a cell expressing the C5 protein with a test compound, and
 CC comparing the levels of C5 expression prior to or after exposure to the
 CC test compound. A difference in expression indicates that the test
 CC compound is a C5 gene expression modulator. The C5 protein (AAY97997,
 CC AAY97999) has sequence similarity with mammalian brown fat uncoupling
 CC protein (UCP). In the exemplifications of the invention, the C5
 CC protein was shown to be able to uncouple ATP synthesis from oxidative
 CC phosphorylation, allowing caloric energy to be dissipated as heat. cDNA
 CC sequences encoding C5 (AAA52253, AAA52254) were isolated in an
 CC investigation to identify genes which are differentially expressed in
 CC body weight disorders such as obesity and cachexia. A compound which
 CC modulates C5 expression is useful for modulating thermogenesis, and is
 CC therefore useful for treating body weight disorders. Increasing the level
 CC of C5 gene expression and/or gene product activity increases the rate of
 CC thermogenesis and causes a reduction in body weight, which is useful for
 CC the treatment of obesity. Decreasing the level of C5 gene expression
 CC and/or C5 gene product activity decreases the rate of thermogenesis
 CC and causes an increase in body weight, which is useful for the treatment
 CC of cachexia. The present sequence represents the human C5 protein.

XX Sequence 309 AA;

Query Match 99.7%; Score 1572; DB 21; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8,2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFATDVPPTATVFKFLGAGTAACTADLTLPDLTAKVRLQIQESQGPVRAVTAQAQR 60
 DB 1 MVGFATDVPPTATVFKFLGAGTAACTADLTLPDLTAKVRLQIQESQGPVRAVTAQAQR 60
 QY 61 GVGTTILMTVRTGPRSLYNGLVAGLQROMSPASVRIGLDSVKQFTYKSGEHSIGSRL 120
 DB 61 GVGTTILMTVRTGPRSLYNGLVAGLQROMSPASVRIGLDSVKQFTYKSGEHSIGSRL 120
 QY 121 LAGSTTGALAVAAQPTDVVKVRFQAQAPAGGRRYOSTVNAVYKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAVAAQPTDVVKVRFQAQAPAGGRRYOSTVNAVYKTIAREEGFRGLMKGTS 180
 QY 181 PNVARNAIVNCAELVTYDLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 DB 181 PNVARNAIVNCAELVTYDLIKALLKANIMTDDLPCQHTSAFGAGFCTTVIASPVYVKT 240
 QY 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVMEVTEQLKRALMA 300
 DB 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMPSPFLRGSNNVMEVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 12
 ID AAY44252 standard; Protein; 309 AA.

XX AAY44252;

XX 28-FEB-2000 (first entry)

DE Human mitochondrial anion carrier, uncoupling protein-2.

XX Mitochondrial uncoupling protein-2; UCP-2; mitochondrial anion carrier;

KW MAC; modulator; transport protein; fatty acid anion; mitochondria;

XX assay vesicle; metabolic disorder; diabetes; obesity; cancer; human.

XX Homo sapiens.

PN W09964458-A1.
 XX 16-DEC-1999.
 XX 08-JUN-1999; 99WO-US12623.
 XX 08-JUN-1998; 98US-0033662.
 XX (UYBO-) UNIV BOSTON.
 XX Corkey BE, Hamilton JA, Pilch PF, Farmer SR, Kirkland JL;
 XX WPI: 2000-087200/07.
 DR N-PSDB; AA229244.
 XX Identifying modulators of mitochondrial anion carriers, potentially
 PT useful for treating metabolic disease, e.g. diabetes and obesity -
 PS Claim 11; Page 71; 80pp; English.
 XX The present sequence is a human uncoupling protein-2
 CC (UCP-2) which is a mitochondrial anion carrier (MAC). The UCPs transport
 CC free fatty acid anions across the inner mitochondrial membrane to induce
 CC cyclical proton movement. This transport is tightly related to oxidation
 CC of fatty acids in the mitochondria, thereby converting fatty acids into
 CC energy rather than storing them. The uncoupling protein is used in the
 CC preparation of assay vesicles that are used to identify modulators of
 CC MAC activity. MAC modulators are useful for treating metabolic disorders,
 CC particularly diabetes and obesity. Modulators that act as inhibitors
 CC can be used to treat conditions requiring a reduction in energy
 CC expenditure, e.g. in cancer patients or the elderly.
 CC
 SQ Sequence 309 AA;
 Query Match 99.7%; Score 1572; DB 21; Length 309;
 Best Local Similarity 99.7%; Pred. No. 8.2e-158;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPTATVVFAGAGTACIADLITFPDITAKVRLQIGESGGPRATASAOYR 60
 DB 1 MGGFKATDVPPTATVVFAGAGTACIADLITFPDITAKVRLQIGESGGPRATASAOYR 60
 QY 61 GWWGTLTINWRTGEPSTLVNGVAGIQRQMSFASVRIQYGVSVQFYTKGSEHASTSRL 120
 DB 61 GWWGTLTINWRTGEPSTLVNGVAGIQRQMSFASVRIQYGVSVQFYTKGSEHASTSRL 120
 QY 121 LAGSTGALAVAVAPPTDVVYKRFQARAGGRRYQSTVNAKYTIAEEGFRGLMKGT 180
 DB 121 LAGSTGALAVAVAPPTDVVYKRFQARAGGRRYQSTVNAKYTIAEEGFRGLMKGT 180
 QY 181 PNVARAIVNCAELVYDILKDALIKANIMTDLCHFTSAFGAGCTTVASVDVYKT 240
 DB 181 PNVARAIVNCAELVYDILKDALIKANIMTDLCHFTSAFGAGCTTVASVDVYKT 240
 QY 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLIGSMNVMMVETVEQLRALMA 300
 DB 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLIGSMNVMMVETVEQLRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 13
 AAM69166
 ID AAM69166 standard; Protein; 309 AA.
 AC AAM69166;

XX 24-NOV-1998 (first entry)
 XX Human respiration uncoupling protein-2 (UCP2).
 DE
 XX

KW Uncoupling protein-2; UCP2 gene; human; respiration;
 KW thermogenesis; obesity; hyperinsulinaemia; glucose intolerance;
 KW diabetes; syndrome X; hypothermia; wasting; cachexia; anorexia;
 KW inflammation; fever; hyperthermia; therapy; diagnosis.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 55
 FT Misc-difference 190 /note= "Val variant results from polymorphism"
 FT Misc-difference 294 /note= "Ser variant results from polymorphism"
 FT Misc-difference 294 /note= "Met variant results from polymorphism"
 XX
 XX W09831396-A1.
 XX 23-JUL-1998.
 XX 22-APR-1997; 97WO-US06864.
 XX 15-JAN-1997; 97US-0034960.
 XX (NAME-) CENT NAT RECH SCI CENT RECH SUR ENDOCRINOL.
 XX (RESC) UNIV CALIFORNIA.
 XX (UYDU-) UNIV DUKE.
 XX Boullaud F, Collins SA, Riquelme D, Seldin MF;
 XX Surwit RS, Warden CH;
 XX WPI: 1998-413823/35.
 DR N-PSDB; AA44595.
 XX
 XX Method for treating disease associated with altered UCP-2 expression
 PT - by administering agent which enhances or inhibits UCP-2 activity,
 PT effectively to treat obesity, diabetes, fever, hyperthermia,
 PT cachexia etc.
 PT
 PS Claim 11; Fig 1a; 98pp; English.
 XX This is the amino acid sequence of a novel human protein,
 CC designated uncoupling protein-2 (UCP2), that is linked to cell
 CC respiration, thermogenesis, obesity and hyperinsulinaemia. The
 CC sequence is deduced from an isolated nucleic acid sequence (see
 CC AA44595). A claimed method for treating a disease or disorder
 CC associated with diminished (or elevated) UCP2 expression or
 CC activity, comprises administering an agent that enhances (or
 CC inhibits) UCP2 expression or activity sufficient to effect the
 CC treatment. Also claimed are: (1) a method for screening a compound
 CC for its ability to modulate UCP2 expression or activity; (2)
 CC isolated mammalian UCP2; (3) an isolated nucleic acid sequence
 CC encoding mammalian UCP2; (4) a recombinant molecule comprising a
 CC vector and the nucleic acid of (3); (5) a host cell that can be
 CC used to produce UCP2; (6) an antibody specific for UCP2; (7) an
 CC antisense construct complementary to UCP2; and (8) a host cell
 CC comprising the construct of (7). An agent which enhances UCP2
 CC expression can be used to treat obesity, diabetes, syndrome X,
 CC hypothermia, hyperinsulinaemia, or glucose intolerance. An
 CC inhibitor of UCP2 is used to treat wasting, anorexia, inflammation,
 CC cachexia, fever or hyperthermia. The constructs of (4) and (7)
 CC can both be used in the method (all claimed). The invention also
 CC relates to diagnostic methodologies.
 CC
 SQ Sequence 309 AA;
 Query Match 99.6%; Score 1570; DB 19; Length 309;
 Best Local Similarity 99.7%; Pred. No. 1.3e-157;
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPTATVVFAGAGTACIADLITFPDITAKVRLQIGESGGPRATASAOYR 60
 DB 1 MGGFKATDVPPTATVVFAGAGTACIADLITFPDITAKVRLQIGESGGPRATASAOYR 60

QY 61 GVMGTTILMTVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTTILMTVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAAOPTDVVAVRFOQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAAOPTDVVAVRFOQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 QY 181 PNVARNALVNCALVLYTDLLKDALIKANLMTDDLPCFFTSAPGAGCTTVIASPVVVKXT 240
 DB 181 PNVARNALVNCALVLYTDLLKDALIKANLMTDDLPCFFTSAPGAGCTTVIASPVVVKXT 240
 QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYTEQLKRALMA 300
 DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 14

AAV28352
 ID AAV28352 standard; protein; 309 AA.

XX AAV28352;

DT 19-OCT-1999 (first entry)

DE UCP2 amino acid sequence (Fleury variant).

XX uncoupling protein; amino acid; mitochondria; diabetes;

KM brown adipose tissue; wild type; obesity; thermo-regulation.

XX Homo sapiens.

PN W09937812-A1.

PD 29-JUL-1999.

PF 21-JAN-1999; 99WC-US01198.

PR 23-JAN-1998; 98US-0012218.

PA (ORCH-) ORCHID BIOCOMPUTER INC.

PI Vrolijk LP;

DR WPI: 1999-469144/39.

DR N-PSDB; AAX99435.

PT A novel single nucleotide polymorphism of the uncoupling protein 2

XX gene, useful for diagnosis, prognosis and treatment of obesity

PS Disclosure; Fig 1; 68pp; English.

XX This is the amino acid sequence of uncoupling protein-2 (UCP-2) as

CC reported by Fleury et al, 1997 Nature genetics.

CC Identifying a UCP2 polymorphism, especially Val55 (thymine at

CC nucleotide 164), can be used to diagnose obesity, non-insulin dependent

CC diabetes mellitus and other UCP2 related diseases (claimed). Wild-type

CC UCP2 generally comprise a cytosine at nucleotide 164 (alanine 55). UCP2

CC related diseases include atherosclerosis, hyperinsulinemia, chronic

CC inflammation, thermogenesis, apoptosis and cachexia.

SQ Sequence 309 AA;

Query Match 99.6%; Score 1570; DB 20; Length 309;

Best Local Similarity 99.7%; Pred. No. 1.3e-157;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPPTATVVKFLGAGTACIADLITPFLDPAKRLQIQESQGPVRAATASQYR 60

DB 1 MNGFKATDVPPPTATVVKFLGAGTACIADLITPFLDPAKRLQIQESQGPVRAATASQYR 60
 QY 61 GVMGTTILMTVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTTILMTVTEGPRSLYNGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAAOPTDVVAVRFOQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAAOPTDVVAVRFOQAPRAGGRRYOSTVNAKYKTIAEEGFRGLMKGTS 180
 QY 181 PNVARNALVNCALVLYTDLLKDALIKANLMTDDLPCFFTSAPGAGCTTVIASPVVVKXT 240
 DB 181 PNVARNALVNCALVLYTDLLKDALIKANLMTDDLPCFFTSAPGAGCTTVIASPVVVKXT 240
 QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYTEQLKRALMA 300
 DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAPFYKGFMPSTLRIGSNVVMVFYTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 15

AAU98901
 ID AAU98901 standard; Protein; 309 AA.

XX AAU98901;

DT 22-AUG-2002 (first entry)

DE Human uncoupling protein UCP-2.

XX Human; uncoupling protein; UCP-2; stroke; ischaemia; epilepsy;

KM neurological disorder; neuronal injury; Parkinson's disease;

KM Huntington's disease; inherited ataxia; motor neuron disease;

KM Alzheimer's disease; traumatic brain injury; Bradykinin;

KM serotonin; histamine; arachidonic acid.

XX Homo sapiens.

PN W0200236829-A2.

PD 10-MAY-2002.

PF 01-NOV-2001; 2001WO-US45744.

PR 01-NOV-2000; 2000US-244946P.

PA (AGYT-) AGY THERAPEUTICS INC.

PI Gonzalez-Zulueta M, Shamloo M, McFarland KC, Chin D, Wieloch T;

DR WPI: 2002-490012/52.

DR N-PSDB; ABK86151.

PT Diagnosing occurrence of stroke or assessing a patient's susceptibility

XX to stroke, by detecting in a patient sample an elevated level of

PS uncoupling proteins-2 expression -

XX Disclosure; Page 79; 80pp; English.

XX The invention relates to a method of diagnosing occurrence of a stroke or

CC assessing a patient's susceptibility to a stroke, comprising detecting in

CC a patient sample an elevated level of uncoupling proteins (UCP)-2

CC expression. The method is useful for diagnosing occurrence of a stroke or

CC assessing a patient's susceptibility to a stroke, where the stroke is an

CC ischaemic stroke. The method is useful for treating a subject having or

CC is susceptible to a neurological disorder or a neuronal injury, where the

CC neuronal injury is a stroke, or an ischaemic stroke. The neurological

CC disorder is selected from Parkinson's disease, Huntington's disease,

CC inherited ataxia, motor neuron disease, Alzheimer's disease, epilepsy,

CC and traumatic brain injury. The disorder is treated with a propylactic
CC agent which increases the permeability of the blood/brain barrier, or
CC with an anticoagulant and a secondary agent selected from bradykinin,
CC serotonin, histamine and arachidonic acid. The agent is a purified
CC UCP-2 polypeptide in combination with an anticoagulant. The method is
CC also useful for screening for an agent useful for treating a neurological
CC disorder or a neuronal injury. The present sequence represents the
CC amino acid sequence of human UCP-2.
XX

SQ Sequence 309 AA;

Query Match 99.6%; Score 1570; DB 23; Length 309;

Best Local Similarity 99.7%; Pred. No. 1.3e-157;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPPTATVVKFLGAGTAACIADLITFPDLTAKVRLIQGESQGPVATASAQYR 60
DB 1 MVGFKATDVPPPTATVVKFLGAGTAACIADLITFPDLTAKVRLIQGESQGPVATASAQYR 60
QY 61 GVMGTILTMVTRTEGPRSLYNGLYAGLCQWMSFASVRLGLDYSVKQFTKGESEHASTGSR 120
DB 61 GVMGTILTMVTRTEGPRSLYNGLYAGLCQWMSFASVRLGLDYSVKQFTKGESEHASTGSR 120
QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREGFRGLWKGT 180
DB 121 LAGSTTGALAAVAVAQPTDVVKVRFQAQARAGGRRYQSTVNAVYKTIAREGFRGLWKGT 180
QY 181 PVARNAALVNCALVLTLDLIDALLKALMTDDLPCHTSAFGAGPCTTVIASPDVYKT 240
DB 181 PVARNAALVNCALVLTLDLIDALLKALMTDDLPCHTSAFGAGPCTTVIASPDVYKT 240
QY 241 RYNSALQGYSSAGHCALTMLQKESPRAFYKGFMSFLRSGMNVVMFVYEQIKRALMA 300
DB 241 RYNSALQGYSSAGHCALTMLQKESPRAFYKGFMSFLRSGMNVVMFVYEQIKRALMA 300
QY 301 ACTSRAPF 309
DB 301 ACTSRAPF 309

Search completed: February 4, 2004, 09:17:59
Job time : 43 secs

Fri Feb 6 16:59:26 2004

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Page 1

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: February 4, 2004, 09:17:09 ; Search time 21 Seconds

(without alignments)
622.574 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576

Sequence: 1 MWGFKATDVPPTATYKFLGA.....TYEOLKRALMACTSRAPF 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

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17: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*

18: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1572	99.7	309	1	US-08-518-878B-51
2	1572	99.7	309	2	US-08-807-861A-51
3	1572	99.7	309	3	US-08-470-868A-51
4	1572	99.7	309	3	US-09-210-681-51
5	1572	99.7	309	3	US-08-946-719A-51
6	1572	99.7	309	4	US-09-547-983-51
7	1520	96.4	299	4	US-08-518-878B-56
8	1520	96.4	299	1	US-08-470-868A-56
9	1282	81.3	303	2	US-08-294-522B-36
10	1279	81.2	303	1	US-08-518-878B-37
11	1279	81.2	303	1	US-08-807-861A-37
12	1279	81.2	303	2	US-08-470-868A-37
13	1279	81.2	303	3	US-09-210-681-37
14	1279	81.2	303	3	US-08-946-719A-37
15	1279	81.2	303	4	US-09-547-983-37
16	1178.5	74.8	308	2	US-08-937-466-2
17	1178.5	74.8	308	2	US-09-172-528-2
18	1178.5	74.8	308	3	US-09-318-199-2
19	1178.5	74.8	308	3	US-09-503-579-2
20	1162.5	73.8	432	2	US-08-937-466-4
21	1162.5	73.8	432	2	US-09-172-528-4
22	1162.5	73.8	432	3	US-09-318-199-4
23	1162.5	73.8	432	3	US-09-503-579-4
24	1149.5	72.9	312	3	US-09-142-565-2
25	967.5	61.4	255	2	US-08-937-466-6
26	967.5	61.4	255	2	US-09-172-528-6
27	967.5	61.4	255	3	US-09-318-199-6

28	967.5	61.4	256	3	US-09-503-579-6	Sequence 6, Appl
29	915.5	58.1	307	2	US-08-807-861A-56	Sequence 56, Appl
30	915.5	58.1	307	3	US-09-210-681-56	Sequence 56, Appl
31	915.5	58.1	307	3	US-08-946-719A-56	Sequence 56, Appl
32	915.5	58.1	307	4	US-09-547-983-56	Sequence 56, Appl
33	894.5	56.8	306	5	PCT-US94-09799-1	Sequence 1, Appl
34	521.5	33.1	335	4	US-09-482-273-118	Sequence 18, App
35	519	32.9	291	4	US-09-501-558-2	Sequence 2, Appl
36	401	25.4	293	4	US-09-501-558-4	Sequence 4, Appl
37	337	21.4	95	3	US-09-142-565-6	Sequence 6, Appl
38	288	18.3	308	4	US-09-599-360B-91	Sequence 91, Appl
39	273	17.3	311	2	US-08-775-009-32	Sequence 32, Appl
40	273	17.3	311	2	US-08-775-009-33	Sequence 32, Appl
41	271	17.2	325	4	US-09-489-847-155	Sequence 155, App
42	256	16.2	320	2	US-08-933-750C-12	Sequence 12, Appl
43	256	16.2	320	3	US-09-234-613-12	Sequence 12, Appl
44	254.5	16.1	298	4	US-09-434-354-49	Sequence 49, Appl
45	252	16.0	74	3	US-09-142-565-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Targila, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518, 878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-51
Query Match 99.7%; Score 1572; DB 1; Length 309;
Local Similarity 99.7%; Pred. No. 4.9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWGFKATDVPPTATYKFLGAGTACIADLLIFPDFAVRILQIGESGSPVRAASQYR 60
DB 1 MWGFKATDVPPTATYKFLGAGTACIADLLIFPDFAVRILQIGESGSPVRAASQYR 60
QY 61 GVGIGTLVWVRTEGRSLVNGLVAGLQROMSPASVRIQLYDSVXQFYTKSEHSAISRL 120

Db 61 GWMGTLTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSEHSAIGSRL 120
Qy 121 LAGSTTGALAAVAAPQPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
Db 121 LAGSTTGALAAVAAPQPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
Qy 181 PNVAENAIVNCALVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
Db 181 PNVAENAIVNCALVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
Qy 241 RYMNSALGOYSSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVVMFVYIEQLKRALMA 300
Db 241 RYMNSALGOYSSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVVMFVYIEQLKRALMA 300
Qy 301 ACTSREAPF 309
Db 301 ACTSREAPF 309

RESULT 2

US-08-807-861A-51
Sequence 51, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITILE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-51

Query Match 99.7%; Score 1572; DB 2; Length 309;
Best Local Similarity 99.7%; Pred. No. 4.9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVGFKATDVPTATVTKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60

Db 1 MVEKATDVPTATVTKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
Qy 61 GWMGTLTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSEHSAIGSRL 120
Db 61 GWMGTLTWRTGPRSLVNGLVAGLQROMSPASVRIGLYDSVKQFTYKSEHSAIGSRL 120
Qy 121 LAGSTTGALAAVAAPQPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
Db 121 LAGSTTGALAAVAAPQPTDVVKRFQAOAGGRRYQSTVNAKYTLAREEGFRGLMKGTS 180
Qy 181 PNVAENAIVNCALVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
Db 181 PNVAENAIVNCALVYTDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPYDVYKT 240
Qy 241 RYMNSALGOYSSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVVMFVYIEQLKRALMA 300
Db 241 RYMNSALGOYSSAGHCALTMLQKGPRAFYKGFMSFLRSGMNVVMFVYIEQLKRALMA 300
Qy 301 ACTSREAPF 309
Db 301 ACTSREAPF 309

RESULT 3

US-08-470-868A-51
Sequence 51, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITILE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-51

Query Match 99.7%; Score 1572; DB 2; Length 309;
Best Local Similarity 99.7%; Pred. No. 4.9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVGFKATDVPTATVTKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
Db 1 MVGFKATDVPTATVTKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60

QY 61 GWMGTLTMTVEGRPSLYNGLVAGLOROMSPASVRIGLYDSVKQFYTKSEHASISRL 120
DB 61 GWMGTLTMTVEGRPSLYNGLVAGLOROMSPASVRIGLYDSVKQFYTKSEHASISRL 120
QY 121 LAGSTTGALAANAQPTDVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAANAQPTDVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNATVNCALVTYDLIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
DB 181 PNVARNATVNCALVTYDLIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
QY 241 RYMNSALQGYSSAGHCALMTLQKEGPRAFYKGFMPSPRLGSMNVNMFVTEYEQKRALMA 300
DB 241 RYMNSALQGYSSAGHCALMTLQKEGPRAFYKGFMPSPRLGSMNVNMFVTEYEQKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 4

US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-210-681-51

Query Match 99.7%; Score 1572; DB 3; Length 309;
Best Local Similarity 99.7%; Pred. No. 4,9e-168;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MUGPRATVPPATATKFLGAGTACIADLTFFPDLTKAVRLQIGSEOGPVRTASAOYR 60
DB 1 MUGPRATVPPATATKFLGAGTACIADLTFFPDLTKAVRLQIGSEOGPVRTASAOYR 60
QY 61 GWMGTLTMTVEGRPSLYNGLVAGLOROMSPASVRIGLYDSVKQFYTKSEHASISRL 120
DB 61 GWMGTLTMTVEGRPSLYNGLVAGLOROMSPASVRIGLYDSVKQFYTKSEHASISRL 120
QY 121 LAGSTTGALAANAQPTDVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAANAQPTDVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNATVNCALVTYDLIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
DB 181 PNVARNATVNCALVTYDLIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVDVYKT 240
QY 241 RYMNSALQGYSSAGHCALMTLQKEGPRAFYKGFMPSPRLGSMNVNMFVTEYEQKRALMA 300
DB 241 RYMNSALQGYSSAGHCALMTLQKEGPRAFYKGFMPSPRLGSMNVNMFVTEYEQKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 5

US-08-946-719A-51
Sequence 51, Application US/08946719A
Patent No. 6121017
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid

Fri Feb 6 16:59:26 2004

us-09-884-814-1.ra1

Page 4

STRANDEDNESS: single
TOPOLOGY: unknown
US-08-946-719A-51

Query Match 99.7%; Score 1572; DB 3; Length 309;
Best Local Similarity 99.7%; Pred. No. 4,9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGFKATDVPPATATKFLGAGTACIADLITFPLDTAKVRLQIQESOGPVATASQYR 60
DB 1 MGFKATDVPPATATKFLGAGTACIADLITFPLDTAKVRLQIQESOGPVATASQYR 60
QY 61 GWMGTLTMTWTEGPRSLNGLVAGLQROMSFASVRIGLYDSVKOPTKSEHASIGSRL 120
DB 61 GWMGTLTMTWTEGPRSLNGLVAGLQROMSFASVRIGLYDSVKOPTKSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPFTDVVKVRFQQAARAGGRRYOSTVNAKYKTAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAPFTDVVKVRFQQAARAGGRRYOSTVNAKYKTAREEGFRGLMKGTS 180
QY 181 PNVAARNAIVNCAELVYTDLIKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
DB 181 PNVAARNAIVNCAELVYTDLIKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
QY 241 RYMNSALGOYSSAGHCHLTMLOKESPRAFYKGFMSFLRSGMNVVMFTYEQLRALMA 300
DB 241 RYMNSALGOYSSAGHCHLTMLOKESPRAFYKGFMSFLRSGMNVVMFTYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 6
US-09-547-983-51

Sequence 51, Application US/09547983
Patent No. 65,8402

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,983
FILING DATE: 12-Apr-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/516,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-547-983-51

Query Match 99.7%; Score 1572; DB 4; Length 309;
Best Local Similarity 99.7%; Pred. No. 4,9e-168;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGFKATDVPPATATKFLGAGTACIADLITFPLDTAKVRLQIQESOGPVATASQYR 60
DB 1 MGFKATDVPPATATKFLGAGTACIADLITFPLDTAKVRLQIQESOGPVATASQYR 60
QY 61 GWMGTLTMTWTEGPRSLNGLVAGLQROMSFASVRIGLYDSVKOPTKSEHASIGSRL 120
DB 61 GWMGTLTMTWTEGPRSLNGLVAGLQROMSFASVRIGLYDSVKOPTKSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAPFTDVVKVRFQQAARAGGRRYOSTVNAKYKTAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAAVAAPFTDVVKVRFQQAARAGGRRYOSTVNAKYKTAREEGFRGLMKGTS 180
QY 181 PNVAARNAIVNCAELVYTDLIKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
DB 181 PNVAARNAIVNCAELVYTDLIKDLKANLMTDLPCHFTSAGAGCTTVIASPVVYKT 240
QY 241 RYMNSALGOYSSAGHCHLTMLOKESPRAFYKGFMSFLRSGMNVVMFTYEQLRALMA 300
DB 241 RYMNSALGOYSSAGHCHLTMLOKESPRAFYKGFMSFLRSGMNVVMFTYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 7
US-08-518-878B-56

Sequence 56, Application US/08518878B
Patent No. 5,702,902

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-8788-56

Query Match 96.4%; Score 1520; DB 1; Length 299;
Best Local Similarity 99.7%; Pred. No. 3.2e-162;
Matches 298; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTATVKFLGAGTACIADLITFPDITAKVRLQIOGSGGPVATASAOYRGVMTILTMV 70
DB 1 PTATVKFLGAGTACIADLITFPDITAKVRLQIOGSGGPVATASAOYRGVMTILTMV 60
QY 71 RTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQPTKGSSEHISRLLAGSTTGALA 130
DB 61 RTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQPTKGSSEHISRLLAGSTTGALA 120
QY 131 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPPVARNALVN 190
DB 121 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPPVARNALVN 180
QY 191 CAELVTYDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYMSALGOY 250
DB 181 CAELVTYDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYMSALGOY 240
QY 251 SSAGHCALTMLQKEGPRAFYKGFMPSEFLRLGSMNVVMFTYEQULKRALMACTSRPAF 309
DB 241 SSAGHCALTMLQKEGPRAFYKGFMPSEFLRLGSMNVVMFTYEQULKRALMACTSRPAF 299

RESULT 8
US-08-470-868A-56
Sequence 56, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF OBESITY: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

Query Match 96.4%; Score 1520; DB 2; Length 299;
Best Local Similarity 99.7%; Pred. No. 1.7e-135;
Matches 264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PTATVKFLGAGTACIADLITFPDITAKVRLQIOGSGGPVATASAOYRGVMTILTMV 70
DB 1 PTATVKFLGAGTACIADLITFPDITAKVRLQIOGSGGPVATASAOYRGVMTILTMV 60
QY 71 RTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQPTKGSSEHISRLLAGSTTGALA 130
DB 61 RTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQPTKGSSEHISRLLAGSTTGALA 120
QY 131 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPPVARNALVN 190
DB 121 VAAOPTDVVKVFQAOARAGGRRYQSTVNAVKTIAREEGFRGLMKGTSPPVARNALVN 180
QY 191 CAELVTYDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYMSALGOY 250
DB 181 CAELVTYDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVVKTRYMSALGOY 240
QY 251 SSAGHCALTMLQKEGPRAFYKGFMPSEFLRLGSMNVVMFTYEQULKRALMACTSRPAF 309
DB 241 SSAGHCALTMLQKEGPRAFYKGFMPSEFLRLGSMNVVMFTYEQULKRALMACTSRPAF 299

RESULT 9
US-08-294-522B-36
Sequence 36, Application US/08294522B
Patent No. 5741666
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF OBESITY: Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-294-522B-36

Query Match 81.3%; Score 1282; DB 1; Length 303;
Best Local Similarity 85.4%; Pred. No. 1.7e-135;
Matches 264; Conservative 12; Mismatches 27; Indels 6; Gaps 6;

QY 1 MWGFRATDVPPATVTKFLGAGTACIADLITFPDITAKVRLQIOGSGGPVATASAOYR 60
DB 1 MWGFRATDVPPATVTKFLGAGTACIADLITFPDITAKVRLQIOGSGGPVATASAOYR 60

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Page 6

QY 61 GVMGTLTMTVTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKSEHASIGSRL 120
DB 61 GVLGTLTMTVTEGPRSLYNGLVAGLQROMSLASVRIGLYDSVKQFYTKSEHGIGSRL 120
QY 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYOSTVNAKYTIAREEGFRLMKGTS 180
DB 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYR-LSISYKNITR-CGIRGLMKGIS 178
QY 181 PNVARNAIYVCAELVYDILKDALIKANIMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 240
DB 179 -QCARNAIYVCAELVYDILKDTLL-SHMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 236
QY 241 RYMSALGOYSAGHCALTMLOKGPRAFYKGFMPSPFLGSMNVVMFVYEQLRALMA 300
DB 237 RYM-TLLGQYHSAGHCALT-CSEBGPALFNQGVMPSPFLGSMNVVMFVYEQLRALMA 294
QY 301 ACTSREAPF 309
DB 295 AVQSRAPF 303

RESULT 10
US-08-518-878B-37
Sequence 37, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518-878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-37

Query Match 81.2%; Score 1279; DB 1; Length 303;
Best Local Similarity 85.1%; Pred. No. 3.7e-135;
Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

QY 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYOSTVNAKYTIAREEGFRLMKGTS 180
DB 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYR-LSISYKNITR-CGIRGLMKGIS 178
QY 181 PNVARNAIYVCAELVYDILKDALIKANIMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 240
DB 179 -QCARNAIYVCAELVYDILKDTLL-SHMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 236
QY 241 RYMSALGOYSAGHCALTMLOKGPRAFYKGFMPSPFLGSMNVVMFVYEQLRALMA 300
DB 237 RYM-TLLGQYHSAGHCALT-CSEBGPALFNQGVMPSPFLGSMNVVMFVYEQLRALMA 294
QY 301 ACTSREAPF 309
DB 295 AVQSRAPF 303

RESULT 11
US-08-807-861A-37
Sequence 37, Application US/08807861A
Patent No. 3853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITILE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-37

Query Match 81.2%; Score 1279; DB 2; Length 303;
Best Local Similarity 85.1%; Pred. No. 3.7e-135;
Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

QY 61 GVMGTLTMTVTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKSEHASIGSRL 120
DB 61 GVLGTLTMTVTEGPRSLYNGLVAGLQROMSLASVRIGLYDSVKQFYTKSEHGIGSRL 120
QY 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYOSTVNAKYTIAREEGFRLMKGTS 180
DB 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYR-LSISYKNITR-CGIRGLMKGIS 178
QY 181 PNVARNAIYVCAELVYDILKDALIKANIMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 240
DB 179 -QCARNAIYVCAELVYDILKDTLL-SHMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 236
QY 241 RYMSALGOYSAGHCALTMLOKGPRAFYKGFMPSPFLGSMNVVMFVYEQLRALMA 300
DB 237 RYM-TLLGQYHSAGHCALT-CSEBGPALFNQGVMPSPFLGSMNVVMFVYEQLRALMA 294
QY 301 ACTSREAPF 309
DB 295 AVQSRAPF 303

QY 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYOSTVNAKYTIAREEGFRLMKGTS 180
DB 121 LAGSTGALAVVAQPTDVVKVFPQAGAGGRRYR-LSISYKNITR-CGIRGLMKGIS 178
QY 181 PNVARNAIYVCAELVYDILKDALIKANIMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 240
DB 179 -QCARNAIYVCAELVYDILKDTLL-SHMTDDLPCHTSAFGAGFCCTIVIASPVDVYKT 236
QY 241 RYMSALGOYSAGHCALTMLOKGPRAFYKGFMPSPFLGSMNVVMFVYEQLRALMA 300
DB 237 RYM-TLLGQYHSAGHCALT-CSEBGPALFNQGVMPSPFLGSMNVVMFVYEQLRALMA 294
QY 301 ACTSREAPF 309
DB 295 AVQSRAPF 303

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Page 7

QY 6 GWNQGITLTWVRREGPSSLVNGLVAGJORMSPASVRIQLYDSVKQFTYKSGEHSIGSRL 120
 Db 61 GVLGTILTWVRREGPSSLVNGLVAGJORMSLASVRIQLYDSVKQFTYKSGEHSIGSRL 120
 QY 121 LAGSTTGALAVVAQPTDVVKYRFGQAPADGGRRPYOSTVNAVYKTAREEGFRGLMKGIS 180
 Db 121 LAGSTTGALAVVAQPTDVVKYRFGCAPGAGGGRPYRA-LSSYNMTR-GGIRGLMKGIS 178
 QY 181 PNVAARAIVNCAELVYDILKDALIKANIMMDLDCHEFTSAFGAGFCCTYIASVDVYKT 240
 Db 179 -QCARAAIVNCAELVYDILKDTLL-SHMTMDLDCHEFTSAFGAGFCCTYIASVDVYKT 236
 QY 241 RYNSAALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRUSMNVMVFVYEQLRALMA 300
 Db 237 RYM-TLLGOYSSAGHCALT-CEEGFALFNQGVMSFLRLSSNMVMVFVYEQLRALMA 294
 QY 301 ACTSREAPF 309
 Db 295 AYQSREAPF 303

RESULT 12
 US-08-470-868A-37
 Sequence 37, Application US/08470868A
 Patent No. 5861485
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis C.
 TITLE OF INVENTION: Compositions and Methods for the
 TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie and Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470, 868A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-0031-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66441 PENNIE
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 303 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 US-08-470-868A-37

Query Match	81.2%;	Score 1279;	DB 2;	Length 303;
Best Local Similarity	85.1%;	Pred. No. 3.7e-135;		
Matches 263;	Conservative 13;	Mismatches 27;	Indels 6;	Gaps 6;

QY MGEFKATDVPATATVYFGLAGFACTAALITFEPDITAKVRLQIQSSQGVATATSAQYR 60

Db 1 MGEFKATDVPATATVYFGLAGFACTAALITFEPDITAKVRLQIQSSQGVATATSAQYR 60

QY 61 GVGATLLNVRLEGPSALYNLVAQLQDMSFAVSRIGLYDSVKQPTKQSEHASTGSHL 120

D6 6. GVLGTLITWVRTEGPRSLYNGLVAGLQJEMSLASVRLIGLVDSVXQFPTKGS EHGIGSRL 120

QY 121 LAGSTTGALAAVVAQPTDVVKYRFPQAQARACGGRRYOSTYNAKYTIAREGPFGLMKGS 180

D6 121 LAGSTTGALAAVVAQPTDVVKYRFPQAPRAGGGRRYRA-LSSYKNITR-GGIGLWKGS 178

QY 181 PNVARAIINCAELVTYDILKDALIKANIMTDDEPCHFTSAFGAFCTTIIASPVVVKI 240

D6 179 -QCARAIINCAELVTYDILKDTLL-SHLMDDDEPCHFTSAFGAFCTTIIASPVVVKI 236

QY 241 RYMSALGOYSAGHCALMTQKCGRAFYGGPMSFLRGSNNVVFVTEQIKRALMA 300

D6 237 RYM-TLLGGYHAGHCALT-CSEEGPALFNQGVMSPLRGSNNVVFVTEQIKRALMA 294

QY 301 ACTSREAPF 309

D6 295 AYQSRAPF 303

RESULT 13
US-09-210-681-37
; Sequence 37, Application US/09210681
; Patent No. 6057109

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF OBESITY
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

1 PRIOR APPLICATION DATA:
 2 APPLICATION NUMBER: 08/807,861
 3 FILING DATE: 26-FEB-1997
 4 APPLICATION NUMBER: US 08/518,878
 5 FILING DATE: 23-AUG-1995
 6 APPLICATION NUMBER: US 08/470,866
 7 FILING DATE: 06-JUN-1995
 8 APPLICATION NUMBER: US 08/294,522
 9 FILING DATE: 23-AUG-1994
 10 ATTORNEY/AGENT INFORMATION:
 11 NAME: Coruzzi, Laura A.
 12 REGISTRATION NUMBER: 30,742
 13 REPRESENTATION NUMBER: 7853-066
 14 TELECOMMUNICATION INFORMATION:
 15 TELEPHONE: (212) 790-9090
 16 TELEFAX: (212) 869-9741/8864
 17 TELETEX: 66141 PENNIE
 18 INFORMATION FOR SEQ ID NO: 37:

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; LENGTH: 303 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

US-09-210-681-37				
Query Match	51.2%	Score 1279;	DB 3;	Length 303;
Best Local Similarity	85.1%	Pred. No. 3.7e+35;		
Matches 26;	Conservative 13;	Mismatches 27;	Indels 6;	Gaps 6;

QY 1 MGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
 Db 1 MGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
 QY 61 GWMGTILMTWRTGPRSLYNGLVAGLQRFQSPASVIRIGLYDSVKQFYTKGSEHAGISRL 120
 Db 61 GVLGTILMTWRTGPRSLYNGLVAGLQRFQSPASVIRIGLYDSVKQFYTKGSEHAGISRL 120
 QY 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQ-LSYKNITR-GGIRGLMKGLS 180
 Db 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQ-LSYKNITR-GGIRGLMKGLS 178
 QY 181 PNVARNAIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSAPGAGFCTTVIASPDVYKT 240
 Db 179 -QCARNAIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSAPGAGFCTTVIASPDVYKT 236
 QY 241 RYNNALGOYSAGHCALTMLOKGPRAFYKGFMPSEFLRGSNNVVMFVYEQLRALMA 300
 Db 237 RYM-TLLGOYHSAGHCALT-CSREGPALFNQGVMPSEFLRGSNNVVMFVYEQLRALMA 294
 QY 301 ACTSREAPF 309
 Db 295 AYQSRAPF 303

RESULT 14

US-08-946-719A-37
 Sequence 37, Application US/08946719A
 Patent No. 6121017

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/946,719A

FILING DATE: 8-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/807,861

FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-107

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELETYPE: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 303 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: unknown

US-08-946-719A-37

Query Match

Best Local Similarity 81.2%; Score 1279; DB 3; Length 303;

Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

QY 1 MGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
 Db 1 MGFKATDVPPATATVFKFLAGTACIADLITFPLDTAKVRLQIQESQGVPRATASQYR 60
 QY 61 GWMGTILMTWRTGPRSLYNGLVAGLQRFQSPASVIRIGLYDSVKQFYTKGSEHAGISRL 120
 Db 61 GVLGTILMTWRTGPRSLYNGLVAGLQRFQSPASVIRIGLYDSVKQFYTKGSEHAGISRL 120
 QY 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQ-LSYKNITR-GGIRGLMKGLS 180
 Db 121 LAGSTTGALAVVAQAQPTDVYKVFQAQADPAGGRRYRQ-LSYKNITR-GGIRGLMKGLS 178
 QY 181 PNVARNAIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSAPGAGFCTTVIASPDVYKT 240
 Db 179 -QCARNAIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSAPGAGFCTTVIASPDVYKT 236
 QY 241 RYNNALGOYSAGHCALTMLOKGPRAFYKGFMPSEFLRGSNNVVMFVYEQLRALMA 300
 Db 237 RYM-TLLGOYHSAGHCALT-CSREGPALFNQGVMPSEFLRGSNNVVMFVYEQLRALMA 294
 QY 301 ACTSREAPF 309
 Db 295 AYQSRAPF 303

RESULT 15

US-09-547-983-37
 Sequence 37, Application US/09547983
 Patent No. 6518402

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/547,983

FILING DATE: 12-APR-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/807,861

FILING DATE: 26-FEB-1997

APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995

APPLICATION NUMBER: US 08/470,868

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Cortuzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7853-066

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELETYPE: 66141 PENNIE

Fri Feb 6 16:59:26 2004

us-09-884-814-1.ral

? INFORMATION FOR SEQ ID NO: 37:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 303 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: unknown
? SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-547-983-37

Query Match 81.2%; Score 1279; DB 4; Length 303;
Best Local Similarity 85.1%; Pred. No. 3.7e-135;
Matches 263; Conservative 13; Mismatches 27; Indels 6; Gaps 6;

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Db 61 GVLGTILMTVRTGPRSLYNGLVAGLQROMSLASVRIGLYDSVKQFTTKGSEHSGSRL 120
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Db 121 IAGSTGALAVAAOPTDVYKVFQAPGAGGRRYRA-LSSYKNITR-GGIRGLMKGLS 178
QY 181 PNVARNAIVNCAELVTTDLIKDALKANTDLDLPGHFTSAFGAGCTTVIASPVVVKT 240
Db 179 -OCARNAIVNCAELVTTDLIKDTLL-SHMTDLDLPGHFTSAFGAGCTTVIASPVVVKT 236
QY 241 RYMNSALGOYSSAGHCALFTLQKEGPRAFYKGFMPSEFLRIGSMNVVMTVTEYQALKALMA 300
Db 237 RYM-TLIGQTHSAGHCALT-CSREGPALFNQGVMPSEFLRIGSMNVVMTVTEYQALRALMA 294
QY 301 ACTSREAPF 309
Db 295 AYOISREAPF 303

Search completed: February 4, 2004, 09:20:29
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:19:29 ; Search time 34 Seconds

(without alignments)
1902.915 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576
Sequence: 1 MWGFKATDVPPRTATVFLGA.....TYEQKRALMACTSRAPF 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1576	100.0	309	US-09-884-814-1	Sequence 1, Appli
2	1576	100.0	309	US-10-270-861-34	Sequence 34, Appli
3	1576	100.0	314	US-10-265-689-1	Sequence 1, Appli
4	1576	100.0	312	US-09-823-886A-4	Sequence 4, Appli
5	1572	99.7	309	US-09-884-814-6	Sequence 6, Appli
6	1570	99.6	309	US-09-884-814-8	Sequence 8, Appli
7	1570	99.6	309	US-10-197-013-3	Sequence 3, Appli
8	1570	99.6	309	US-10-001-051B-2	Sequence 2, Appli
9	1145.5	72.9	312	US-09-734-134-2	Sequence 2, Appli
10	1145.5	72.9	312	US-09-826-507-2	Sequence 2, Appli
11	1145.5	72.9	312	US-09-808-457-2	Sequence 2, Appli
12	1101.5	69.9	300	US-10-270-861-35	Sequence 35, Appli
13	998.5	63.4	275	US-09-808-457-4	Sequence 4, Appli
14	998.5	63.4	284	US-09-823-886A-6	Sequence 6, Appli
15	915	58.1	307	US-09-823-886A-2	Sequence 2, Appli

16	907	57.6	307	US-10-270-861-33	Sequence 33, Appli
17	521.5	33.1	322	US-10-270-861-7	Sequence 7, Appli
18	521.5	33.1	325	US-10-270-861-1	Sequence 1, Appli
19	521.5	33.1	335	US-09-984-271-118	Sequence 118, App
20	517.5	32.8	322	US-10-270-861-11	Sequence 11, Appli
21	517.5	32.8	325	US-10-270-861-13	Sequence 13, Appli
22	510	32.4	291	US-10-108-260A-2476	Sequence 2476, App
23	486	31.5	353	US-10-270-861-9	Sequence 9, Appli
24	473.5	30.0	323	US-09-946-377A-406	Sequence 406, App
25	473.5	30.0	323	US-10-015-387A-406	Sequence 406, App
26	473.5	30.0	323	US-10-063-735-126	Sequence 126, App
27	473.5	30.0	323	US-10-006-130A-406	Sequence 406, App
28	473.5	30.0	323	US-10-006-172A-406	Sequence 406, App
29	473.5	30.0	323	US-10-015-392A-406	Sequence 406, App
30	473.5	30.0	323	US-10-017-253A-406	Sequence 406, App
31	473.5	30.0	323	US-10-017-306A-406	Sequence 406, App
32	473.5	30.0	323	US-10-063-526-126	Sequence 126, App
33	473.5	30.0	323	US-10-063-586-126	Sequence 126, App
34	473.5	30.0	323	US-10-012-664A-406	Sequence 406, App
35	473.5	30.0	323	US-10-017-867A-406	Sequence 406, App
36	473.5	30.0	323	US-10-063-514-126	Sequence 126, App
37	473.5	30.0	323	US-10-063-514-126	Sequence 126, App
38	473.5	30.0	323	US-10-063-516-126	Sequence 126, App
39	473.5	30.0	323	US-10-063-523-126	Sequence 126, App
40	473.5	30.0	323	US-10-063-527-126	Sequence 126, App
41	473.5	30.0	323	US-10-063-528-126	Sequence 126, App
42	473.5	30.0	323	US-10-063-529-126	Sequence 126, App
43	473.5	30.0	323	US-10-063-536-126	Sequence 126, App
44	473.5	30.0	323	US-10-063-540-126	Sequence 126, App
45	473.5	30.0	323	US-10-063-546-126	Sequence 126, App

ALIGNMENTS

RESULT 1
US-09-884-814-1
Sequence 1, Application US/09884814
Patent No. US20020127600A1
GENERAL INFORMATION:
APPLICANT: Chen, Jin-Long
APPLICANT: Amarel, M. Catherine
TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and Methods of Use
FILE REFERENCE: 018781-00110US
CURRENT APPLICATION NUMBER: US/09/884,814
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 09/124,293
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tulaxix)
US-09-884-814-1
Query Match 100.0%; Score 1576; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 3.3e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWGFKATDVPPRTATVFLGAGTAACIADITPPLDTAKRLQIQESGQPYRATASQYR 60
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DB 181 PNVARNAINVCAELVTYDILIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVVVK 240
QY 241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
DB 241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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RESULT 2

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US-10-270-861-34
; Sequence 34, Application US/10270861
; Publication No. US2003007749A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Pan, James
; TITLE OF INVENTION: UCPS
; FILE REFERENCE: P1663R2
; CURRENT APPLICATION NUMBER: US/10/270,861
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/433,622
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/110,286
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/129,583
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: US 60/143,886
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 34
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-270-861-34

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Query Match      100.0%; Score 1576; DB 15; Length 309;
Best Local Similarity 100.0%; Pred. No. 3,3e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MWGFKATDVPTATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESQGPVATASAOYR 60
DB 1 MWGFKATDVPTATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESQGPVATASAOYR 60
QY 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVQFTYKSEHASISRL 120
DB 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVQFTYKSEHASISRL 120
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QY 181 PNVARNAINVCAELVTYDILIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVVVK 240
DB 181 PNVARNAINVCAELVTYDILIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVVVK 240
QY 241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
DB 241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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RESULT 3
US-10-265-689-1

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; Sequence 1, Application US/10265689
; Publication No. US2003011975A1
; GENERAL INFORMATION:
; APPLICANT: SURMIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICOUIER, DANIEL
; APPLICANT: BOUILLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-265-689-1

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Best Local Similarity 100.0%; Pred. No. 3,3e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MWGFKATDVPTATVKEFLGAGTAACIADLITFPLDTAKVRLQIQESQGPVATASAOYR 60
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DB 61 GVMGTILTMVTEGPRSLVNGLVAGLQROMSFASVRIGLYDSVQFTYKSEHASISRL 120
QY 121 LAGSTTGALAVAVAOPTDVVKRFQAOARAGGRKRYOSTVNAKYTTIAREEGFGLMKGS 180
DB 121 LAGSTTGALAVAVAOPTDVVKRFQAOARAGGRKRYOSTVNAKYTTIAREEGFGLMKGS 180
QY 181 PNVARNAINVCAELVTYDILIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVVVK 240
DB 181 PNVARNAINVCAELVTYDILIKDALLKANLMTDDLPCHTSAFGAGCTTVIASPVVVK 240
QY 241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
DB 241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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RESULT 4
US-09-823-886A-4
; Sequence 4, Application US/09823886A
; Publication No. US20030150022A1
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha
; APPLICANT: Berry-Lowe, Sandra
; TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
; FILE REFERENCE: C1102/7002
; CURRENT APPLICATION NUMBER: US/09/823,886A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,553
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 314

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-814-4
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Best Local Similarity 100.0%; Pred. No. 3,4e-157;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GVMGTILTMVRTGSPRLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
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DB 186 PNVARNAIVNCAELVTVYDLIKALLKANLMTDDLPCHFSTAGAGFCTTVIASPVYVYKT 245
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DB 246 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVVMFVYEQIKRALMA 305
QY 301 ACTSREAPF 309
DB 306 ACTSREAPF 314

RESULT 5
US-09-884-814-6
; Sequence 6, Application US/09884814
; Patent No. US20020127600A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-001110US
; CURRENT APPLICATION NUMBER: US/09/884,814
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Tartaglia et al.
US-09-884-814-6
Query Match          99.7%; Score 1572; DB 10; Length 309;
Best Local Similarity 99.7%; Pred. No. 8,7e-157;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKRRLQIQESQGPVRAATASQYR 60
DB 1 MNGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKRRLQIQESQGPVRAATASQYR 60
QY 61 GVMGTILTMVRTGSPRLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVMGTILTMVRTGSPRLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAVAAVAPPTDVYKVFQQAAPAGGRRYQSTVNAKYKTIASEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAVAPPTDVYKVFQQAAPAGGRRYQSTVNAKYKTIASEGFRGLMKGTS 180
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QY 181 PNVARNAIVNCAELVTVYDLIKALLKANLMTDDLPCHFSTAGAGFCTTVIASPVYVYKT 240
DB 181 PNVARNAIVNCAELVTVYDLIKALLKANLMTDDLPCHFSTAGAGFCTTVIASPVYVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVVMFVYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVVMFVYEQIKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 6
US-09-884-814-8
; Sequence 8, Application US/09884814
; Patent No. US20020127600A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-001110US
; CURRENT APPLICATION NUMBER: US/09/884,814
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Fleury et al.
US-09-884-814-8
Query Match          99.6%; Score 1570; DB 10; Length 309;
Best Local Similarity 99.7%; Pred. No. 1,4e-156;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNGFKATDVPPTATVFKFLGAGTACIADLITPPLDTAKRRLQIQESQGPVRAATASQYR 60
QY 61 GVMGTILTMVRTGSPRLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVMGTILTMVRTGSPRLNGVLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAVAAVAPPTDVYKVFQQAAPAGGRRYQSTVNAKYKTIASEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAVAPPTDVYKVFQQAAPAGGRRYQSTVNAKYKTIASEGFRGLMKGTS 180
QY 181 PNVARNAIVNCAELVTVYDLIKALLKANLMTDDLPCHFSTAGAGFCTTVIASPVYVYKT 240
DB 181 PNVARNAIVNCAELVTVYDLIKALLKANLMTDDLPCHFSTAGAGFCTTVIASPVYVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVVMFVYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKGPRAFYKGFMPSPFLRGSNNVVMFVYEQIKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 7
US-10-197-019-3
; Sequence 3, Application US/10,97019
; Publication No. US20030207284A1
; GENERAL INFORMATION:
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; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher Raleigh
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE
; FILE REFERENCE: MMH-0042US
; CURRENT APPLICATION NUMBER: US/10/197,019
; PRIORITY FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: PCT/US01/02485
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-197-019-3

Query Match          99.6%; Score 1570; DB 12; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.4e-156;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGKATDVPPPTATVTFKFLGAGTACIADLITPDLTAKRLOIQESGQPVATASQYR 60
DB 1 MGGKATDVPPPTATVTFKFLGAGTACIADLITPDLTAKRLOIQESGQPVATASQYR 60
QY 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRLMKGTS 180
DB 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRLMKGTS 180
QY 181 PNVARNAIVNCAELVYDILKDALIKANLMTDDLPCHEFSAFGACFTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCAELVYDILKDALIKANLMTDDLPCHEFSAFGACFTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRIGSWNVVMEVYEQLRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRIGSWNVVMEVYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 8
US-10-001-051B-2
; Sequence 2, Application US/10001051B
; Publication No. US20020172558A1
; GENERAL INFORMATION:
; APPLICANT: Gonzalez-Zulueta, Mirella
; APPLICANT: Shamloo, Mehdiad
; APPLICANT: McFarland, K.C.
; APPLICANT: Chin, Daniel
; APPLICANT: Wielech, Tadeusz
; APPLICANT: Melcher, Thorsten
; APPLICANT: AGY Therapeutics, Inc.
; TITLE OF INVENTION: METHODS OF DIAGNOSING, PREVENTING AND TREATING
; TITLE OF INVENTION: NEUROLOGICAL DISORDERS AND NEURONAL INJURIES
; FILE REFERENCE: 019488-003010US
; CURRENT APPLICATION NUMBER: US/10/001,051B
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/244,946
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Unknown Organism

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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Any animal
; OTHER INFORMATION: source, typically mammalian, most typically human
; US-10-001-051B-2

Query Match          99.6%; Score 1570; DB 14; Length 309;
Best Local Similarity 99.7%; Pred. No. 1.4e-156;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGGKATDVPPPTATVTFKFLGAGTACIADLITPDLTAKRLOIQESGQPVATASQYR 60
DB 1 MGGKATDVPPPTATVTFKFLGAGTACIADLITPDLTAKRLOIQESGQPVATASQYR 60
QY 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRLMKGTS 180
DB 121 LAGSTTGALAAVAAGPTDVVKRFPQAQAAGGRRYOSTVNAVYKTIAREEGFRLMKGTS 180
QY 181 PNVARNAIVNCAELVYDILKDALIKANLMTDDLPCHEFSAFGACFTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCAELVYDILKDALIKANLMTDDLPCHEFSAFGACFTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRIGSWNVVMEVYEQLRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFLRIGSWNVVMEVYEQLRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 9
US-09-734-134-2
; Sequence 2, Application US/09734134
; Patent No. US20010010929A1
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James Godden
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002-D1
; CURRENT APPLICATION NUMBER: US/09/734,134
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: GB 9704551.2
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: GB 9705614.7
; PRIOR FILING DATE: 1997-03-18
; PRIOR APPLICATION NUMBER: EP 97305305.1
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: GB 9800633
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 09/142,565
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-734-134-2

Query Match          72.2%; Score 1149.5; DB 9; Length 312;
Best Local Similarity 72.2%; Pred. No. 2.5e-112;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

QY 1 MGGKATDVPPPTATVTFKFLGAGTACIADLITPDLTAKRLOIQESGQPVATASQYR 60
DB 1 MGGKATDVPPPTATVTFKFLGAGTACIADLITPDLTAKRLOIQESGQPVATASQYR 59
QY 61 GWMGTILTWRTGPRSLYNGLVAGLQRMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 119

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Db      60 GVLGTLTMTVRTEGCSFYNGLVAGLQROMSFASIRILGYSVQVYTPKCADNSLTLTR 119
      120 LLAGSTTGALAAVAVOPTDVVVRFOQAARAG---GGRYOSTYNAVYKTIAREEGFGLM 176
      120 LLAGCTTGAMAVTCQAPTDVVVRFOASIHGSPSRDKYSIGTMDAKRTIAREEGVAGLM 179
Qy      177 KGTSPVNAENAIIVNCAELVYTDILKDALIKANLMTDLPCHFTSAFGAGFCTTVIASPVD 236
      180 KGTLPINMNAIIVNCAEVYTDILKEKLDLHDNLPCHFTSAFGAGFCAIVVASPVD 239
Db      237 VKTRYNMSALGOYSAGHCALTMLOKEGPRAPFYKGMPSFLRLGSMNVVVFVTEQLKR 296
      240 VKTRYNMSPPGQYFSPDLCMIKMYAOEGPTAFYKGFPSFLRLGSMNVVVFVTEQLKR 299
Qy      297 ALMAACTSREAPF 309
      300 ALMKVQMLRESPE 312

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RESULT 10

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US-09-826-507-2
; Sequence 2, Application US/09826507
; Patent No. US20020004492A1
; GENERAL INFORMATION:
; APPLICANT: Lee James Beasley
; APPLICANT: Robert James Godden
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: GH-90009-C1
; CURRENT APPLICATION NUMBER: US/09/826,507
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/312,620
; PRIOR FILING DATE: 1998-05-17
; PRIOR APPLICATION NUMBER: 9814926.3
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 312
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-507-2

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Query Match      72.9%; Score 1149.5; DB 9; Length 312;
Best Local Similarity 72.2%; Pred. No. 2.5e-112;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

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Qy      1 MNGFATDVPPTAVKFLGAGTACIADLITPPLDTAKVLOIGESOGPYRATASAOYR 60
      1 MNGLKPSDVPPTMAVKEFLGAGTACFADLVTFPLDTAKVLOIGENQA-VQYRLVQYR 59
Db      61 GVMGTLTMTVRTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
      60 GVLGTLTMTVRTEGPRSLYNGLVAGLQROMSFASIRILGYDSVQVYTPKCADNSLTLTR 119
Qy      120 LLAGSTTGALAAVAVOPTDVVVRFOQAARAG---GGRYOSTYNAVYKTIAREEGFGLM 176
      120 LLAGCTTGAMAVTCQAPTDVVVRFOASIHGSPSRDKYSIGTMDAKRTIAREEGVAGLM 179
Db      177 KGTSPVNAENAIIVNCAELVYTDILKDALIKANLMTDLPCHFTSAFGAGFCTTVIASPVD 236
      180 KGTLPINMNAIIVNCAEVYTDILKEKLDLHDNLPCHFTSAFGAGFCAIVVASPVD 239
Qy      237 VKTRYNMSALGOYSAGHCALTMLOKEGPRAPFYKGMPSFLRLGSMNVVVFVTEQLKR 296
      240 VKTRYNMSPPGQYFSPDLCMIKMYAOEGPTAFYKGFPSFLRLGSMNVVVFVTEQLKR 299
Qy      297 ALMAACTSREAPF 309
      300 ALMKVQMLRESPE 312

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RESULT 11

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US-09-808-457-2
; Sequence 2, Application US/09808457
; Patent No. US20020065239A1
; GENERAL INFORMATION:
; APPLICANT: Boettcher, Brian
; APPLICANT: Caplan, Shari
; APPLICANT: Kaleko, Michael
; APPLICANT: Connolly, Sheila
; APPLICANT: Desai, Urvil
; APPLICANT: Sloberg, Eric
; TITLE OF INVENTION: Methods and Compositions for Treatment
; TITLE OF INVENTION: of Diabetes and Related Conditions Via Gene Therapy
; FILE REFERENCE: 4:3133A/US
; CURRENT APPLICATION NUMBER: US/09/808,457
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/xxx,xxx
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 312
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Protein UCP3L
US-09-808-457-2

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Query Match      72.9%; Score 1149.5; DB 9; Length 312;
Best Local Similarity 72.2%; Pred. No. 2.5e-112;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

```

```

Qy      1 MNGFATDVPPTAVKFLGAGTACIADLITPPLDTAKVLOIGESOGPYRATASAOYR 60
      1 MNGLKPSDVPPTMAVKEFLGAGTACFADLVTFPLDTAKVLOIGENQA-VQYRLVQYR 59
Db      61 GVMGTLTMTVRTEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
      60 GVLGTLTMTVRTEGCSFYNGLVAGLQROMSFASIRILGYDSVQVYTPKCADNSLTLTR 119
Qy      120 LLAGSTTGALAAVAVOPTDVVVRFOQAARAG---GGRYOSTYNAVYKTIAREEGFGLM 176
      120 LLAGCTTGAMAVTCQAPTDVVVRFOASIHGSPSRDKYSIGTMDAKRTIAREEGVAGLM 179
Db      177 KGTSPVNAENAIIVNCAELVYTDILKDALIKANLMTDLPCHFTSAFGAGFCTTVIASPVD 236
      180 KGTLPINMNAIIVNCAEVYTDILKEKLDLHDNLPCHFTSAFGAGFCAIVVASPVD 239
Qy      237 VKTRYNMSALGOYSAGHCALTMLOKEGPRAPFYKGMPSFLRLGSMNVVVFVTEQLKR 296
      240 VKTRYNMSPPGQYFSPDLCMIKMYAOEGPTAFYKGFPSFLRLGSMNVVVFVTEQLKR 299
Qy      297 ALMAACTSREAPF 309
      300 ALMKVQMLRESPE 312

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RESULT 12
US-10-270-861-35
; Sequence 35, Application US/10270861
; Publication No. US2003007749A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Sean
; APPLICANT: Pan, James
; TITLE OF INVENTION: UCPS
; FILE REFERENCE: P166382
; CURRENT APPLICATION NUMBER: US/10/270,861
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US/09/433,622
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: US 60/110,286
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/129,583

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PRIOR FILING DATE: 1999-04-16
 PRIOR APPLICATION NUMBER: US 60/143,886
 PRIOR FILING DATE: 1999-07-15
 NUMBER OF SEQ ID NOS: 36
 SEQ ID NO 35
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-270-861-35

Query Match 69.9%; Score 1101.5; DB 15; Length 300;
 Best Local Similarity 72.6%; Pred. No. 2.7e-107;
 Matches 217; Conservative 30; Mismatches 47; Indels 5; Gaps 3;

QY 15 VFELGAGTAACIADITLTPPLDTAKVRLQIGESGQPVATASQYRGWMTITLWRTG 74
 DB 3 VFELGAGTAACIADITLTPPLDTAKVRLQIGESGQPVATASQYRGWMTITLWRTG 61
 QY 75 PSLVNGIYAGLQROMSFASVIRIGLYDSVKQFYT-KGSEHASIGSRLLAGSTTGALAVY 133
 DB 62 PCSYNGIYAGLQROMSFASIRIGLYDSVKQYTPKGDNSLITRILACCTGAMAVTC 121
 QY 134 AOPTVVKRFQAGARAG---GGRYQSTVNAKYTIAEEGFRGIMGSPNVAALYN 190
 DB 122 AOPTVVKRFQASIHLPGRSDRKYSGTMDAYRTIAEEGVRGLMGTLPNTRNALYN 181
 QY 191 CAELVYDILKDALIKANIMTDDLPCHFSTAFGAGFCTTVIASPDVVKTRYNSALGOY 250
 DB 182 CAELVYDILKDALIKANIMTDDLPCHFSTAFGAGFCTTVIASPDVVKTRYNSALGOY 241
 QY 251 SSAGHCALTMLOKEPRAPFYKGFMSFRLGSSNVMVVFYEQKRALMACSREAPF 309
 DB 242 FSPDCKIMVAQEGPTAFYKGFMSFRLGSSNVMVVFYEQKRALMACSREAPF 300

RESULT 13

US-09-808-457-4
 Sequence 4, Application US/09808457
 Patent No. US20020065239A1
 GENERAL INFORMATION:
 APPLICANT: Boettcher, Brian
 APPLICANT: Caplan, Shari
 APPLICANT: Kaleko, Michael
 APPLICANT: Connelly, Sheila
 APPLICANT: Desai, Urvy
 APPLICANT: Siosbery, Eric
 TITLE OF INVENTION: Methods and Compositions for Treatment
 FILE REFERENCE: 4-31353A/USN
 CURRENT APPLICATION NUMBER: US/09/808,457
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/XXX,XXX
 PRIOR FILING DATE: 2000-03-15
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 275
 TYPE: PRT
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Protein UCP35
 US-09-808-457-4

Query Match 63.4%; Score 998.5; DB 9; Length 275;
 Best Local Similarity 71.0%; Pred. No. 1.6e-96;
 Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY 1 MGFKATDVPPPTATVYKFLGAGTAACIADITLTPPLDTAKVRLQIGESGQPVATASQYR 60
 DB 1 MGFKATDVPPPTATVYKFLGAGTAACIADITLTPPLDTAKVRLQIGESGQPVATASQYR 59
 QY 61 GVGITLITWRTGSPSYNGIYAGLQROMSFASVIRIGLYDSVKQFYT-KGSEHASIGSR 119

DB 60 GVLGTLITWRTGSPSYNGIYAGLQROMSFASIRIGLYDSVKQYTPKGDNSLITR 119
 QY 120 LLAGSTTGALAVAAQPTDVYKRFQAGARAG---GGRYQSTVNAKYTIAEEGFRGLM 176
 DB 120 LLAGSTTGALAVAAQPTDVYKRFQASIHLPGRSDRKYSGTMDAYRTIAEEGVRGLM 179
 QY 177 KGTSPNVAALYNCAELVYDILKDALIKANIMTDDLPCHFSTAFGAGFCTTVIASPDV 236
 DB 180 KGTLPNTRNALYNCAELVYDILKDALIKANIMTDDLPCHFSTAFGAGFCTTVIASPDV 239
 QY 237 VVKTRYNSALGOYSSAGHCALTMLOKEPRAPFYKG 272
 DB 240 VVKTRYNSALGOYSSAGHCALTMLOKEPRAPFYKG 275

RESULT 14

US-09-823-886A-6
 Sequence 6, Application US/09823886A
 Publication No. US20030150022A1
 GENERAL INFORMATION:
 APPLICANT: Newell, Martha
 APPLICANT: Berry-Lowe, Sandra
 TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
 FILE REFERENCE: C1102/7002
 CURRENT APPLICATION NUMBER: US/09/823,886A
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: US 60/193,533
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 6
 LENGTH: 284
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-823-886A-6

Query Match 63.4%; Score 998.5; DB 12; Length 284;
 Best Local Similarity 71.0%; Pred. No. 1.7e-96;
 Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

QY 1 MGFKATDVPPPTATVYKFLGAGTAACIADITLTPPLDTAKVRLQIGESGQPVATASQYR 60
 DB 10 MGFKATDVPPPTATVYKFLGAGTAACIADITLTPPLDTAKVRLQIGESGQPVATASQYR 68
 QY 61 GVGITLITWRTGSPSYNGIYAGLQROMSFASVIRIGLYDSVKQFYT-KGSEHASIGSR 119
 DB 69 GVGITLITWRTGSPSYNGIYAGLQROMSFASIRIGLYDSVKQYTPKGDNSLITR 128
 QY 120 LLAGSTTGALAVAAQPTDVYKRFQAGARAG---GGRYQSTVNAKYTIAEEGFRGLM 176
 DB 129 LLAGSTTGALAVAAQPTDVYKRFQASIHLPGRSDRKYSGTMDAYRTIAEEGVRGLM 188
 QY 177 KGTSPNVAALYNCAELVYDILKDALIKANIMTDDLPCHFSTAFGAGFCTTVIASPDV 236
 DB 189 KGTLPNTRNALYNCAELVYDILKDALIKANIMTDDLPCHFSTAFGAGFCTTVIASPDV 248
 QY 237 VVKTRYNSALGOYSSAGHCALTMLOKEPRAPFYKG 272
 DB 249 VVKTRYNSALGOYSSAGHCALTMLOKEPRAPFYKG 284

RESULT 15

US-09-823-886A-2
 Sequence 2, Application US/09823886A
 Publication No. US20030150022A1
 GENERAL INFORMATION:
 APPLICANT: Newell, Martha
 APPLICANT: Berry-Lowe, Sandra
 TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
 FILE REFERENCE: C1102/7002
 CURRENT APPLICATION NUMBER: US/09/823,886A
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: US 60/193,533

; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 307
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-823-886A-2

Query Match 58.1%; Score 915; DB 12; Length 307;
 Best Local Similarity 59.3%; Pred. No. 1.2e-87;
 Matches 178; Conservative 48; Mismatches 68; Indels 6; Gaps 3;

Qy	1	MVGFKADVPPTATVFLGAGTACTADLTFFLDTAQVRLQIGESGCPVATASQYR	60
Db	1	MGGLTASDVHPTLGVQLFSAGIACTADVITFPLDTAKVRLQVQSCP---TSSVIRYK	56
Qy	61	GVNGTILTMVRTGPRSLYNGLVAGLQKQSPASVRIGLYDSVKQFYTKSEHA-SIGSR	119
Db	57	GVIGTITAVVKTGSRMKLYSGLPAGLQKQISSASLRIGLYDTVQEFITAGKETAPSLGSK	116
Qy	120	LLAGSTGALAVVAQPTDYVYKRFQQAARAGGR-RYOSTVNAKXITIRKEGFRGLMKG	178
Db	117	LLAGLTGGVAVFVIGQTEVYKVRLOAQSHLHGIXPRYGTYNARILATTEGLTGLMKG	176
Qy	179	TSPVARNATVNCALVYTDLIDKALLKANLMTDLPCHFTSAFGAGFCTTVIASPVDVY	238
Db	177	TTPPLMRSVIINCETELVYDLMKEAFVKNITLADVPCHLVSAALLAGFCATMSSPVDVY	236
Qy	239	KTRYMNSALQYSSAGHCALTMLOKEGPRAFYKGFMSFLRLGSNNVVMFVYEQLRAL	298
Db	237	KTRFINSPPGQYKSVPCAMKVFTEGPTAFKGLVPSFLRLGSNNVIMFVCFEQLRKL	296

Search completed: February 4, 2004, 09:24:59
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:18:04 ; Search time 175 Seconds

(without alignments)
1606.657 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576
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Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pending Patents AA Main:*

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3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	1576	100.0	309	1	PCT-US99-01198-1	Sequence 1, Appl
3	1576	100.0	309	1	PCT-US99-06311-3	Sequence 3, Appl
4	1576	100.0	309	1	PCT-US99-17246-2	Sequence 2, Appl
5	1576	100.0	309	14	US-09-012-218-1	Sequence 1, Appl
6	1576	100.0	309	15	US-09-124-293-2	Sequence 2, Appl
7	1576	100.0	309	16	US-09-277-575-8	Sequence 8, Appl
8	1576	100.0	309	17	US-09-353-645-1	Sequence 1, Appl
9	1576	100.0	309	18	US-09-433-622-34	Sequence 34, Appl
10	1576	100.0	309	19	US-09-599-760-4	Sequence 4, Appl
11	1576	100.0	309	21	US-09-711-022-8	Sequence 8, Appl
12	1576	100.0	309	21	US-09-743-847-4	Sequence 4, Appl
13	1576	100.0	309	21	US-09-743-847-4	Sequence 4, Appl
14	1576	100.0	309	23	US-09-884-814-1	Sequence 1, Appl
15	1576	100.0	309	28	US-10-265-689-1	Sequence 1, Appl
16	1576	100.0	309	28	US-10-270-861-34	Sequence 34, Appl
17	1576	100.0	309	29	US-10-336-472-132	Sequence 132, App
18	1576	100.0	309	31	US-10-631-467-884	Sequence 884, App
19	1576	100.0	309	32	US-60-453-050-13010	Sequence 13010, A
20	1576	100.0	309	32	US-60-453-135-13010	Sequence 13010, A
21	1576	100.0	309	32	US-60-455-444-6960	Sequence 6960, Ap
22	1576	100.0	309	32	US-60-465-241-6960	Sequence 6960, Ap
23	1576	100.0	309	32	US-60-466-412-13010	Sequence 13010, A
24	1576	100.0	314	23	US-09-823-886A-4	Sequence 4, Appl
25	1576	100.0	337	24	US-09-949-016-9410	Sequence 9410, Ap
26	1572	99.7	309	1	PCT-US99-01198-3	Sequence 3, Appl
27	1572	99.7	309	1	PCT-US99-12623-4	Sequence 4, Appl
28	1572	99.7	309	1	PCT-US99-17246-6	Sequence 6, Appl
29	1572	99.7	309	8	US-08-470-868-51	Sequence 51, Appl
30	1572	99.7	309	9	US-08-518-878A-51	Sequence 51, Appl
31	1572	99.7	309	12	US-08-807-861-51	Sequence 51, Appl
32	1572	99.7	309	13	US-08-946-719-51	Sequence 51, Appl
33	1572	99.7	309	14	US-09-012-218-3	Sequence 3, Appl
34	1572	99.7	309	14	US-09-093-662-4	Sequence 4, Appl
35	1572	99.7	309	15	US-09-124-293-6	Sequence 6, Appl
36	1572	99.7	309	17	US-09-397-342-17	Sequence 17, Appl
37	1572	99.7	309	17	US-09-397-342A-17	Sequence 17, Appl
38	1572	99.7	309	17	US-09-397-342B-17	Sequence 17, Appl
39	1572	99.7	309	23	US-09-884-814-6	Sequence 6, Appl
40	1570	99.6	309	1	PCT-US99-01198-2	Sequence 2, Appl
41	1570	99.6	309	1	PCT-US99-17246-8	Sequence 8, Appl
42	1570	99.6	309	14	US-09-012-218-2	Sequence 2, Appl
43	1570	99.6	309	15	US-09-124-293-8	Sequence 8, Appl
44	1570	99.6	309	23	US-09-884-814-8	Sequence 8, Appl
45	1570	99.6	309	26	US-10-001-051B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
PCT-US03-00253-132
Sequence 132, Application PC/TUS0300253
GENERAL INFORMATION:
APPLICANT: Carigen Corp. et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-533C-061 (CURA 833C WO)
CURRENT APPLICATION NUMBER: PCT/US03/00253
PRIOR FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: 10/336,472
PRIOR FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 10/080,334
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/092,900
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 10/136,826
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 10/236,417
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/345,092
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/345,219
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/348,804

PRIOR FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: 60/349,182
 PRIOR FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: 60/349,733
 PRIOR FILING DATE: 2002-01-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 230
 SOFTWARE: Cuiaseq1st version 0.1
 SEQ ID NO 132
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US03-00253-132

Query Match 100.0%; Score 1576; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.8e-159;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPATATVKEFLGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 DB 1 MGGFKATDVPPATATVKEFLGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 QY 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 DB 181 PNVARNALVNCALVTVYDILKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 DB 181 PNVARNALVNCALVTVYDILKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYMNSALGOYSAGHCALITMLQKGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMNSALGOYSAGHCALITMLQKGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 2
 PCT-US99-01198-1
 Sequence 1, Application PC/TUS9901198
 GENERAL INFORMATION:
 APPLICANT: Picoult-Vrolijk, Leslie
 TITLE OF INVENTION: Single Nucleotide Polymorphisms of the
 TITLE OF INVENTION: Uncoupling Protein 2 (UCP2) Gene
 FILE REFERENCE: 04990.0048
 CURRENT APPLICATION NUMBER: PCT/US99/01198
 CURRENT FILING DATE: 1999-01-21
 EARLIER APPLICATION NUMBER: 09/012,21
 EARLIER FILING DATE: 1998-01-23
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Homo sapiens
 PCT-US99-01198-1

Query Match 100.0%; Score 1576; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.8e-159;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPATATVKEFLGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 DB 1 MGGFKATDVPPATATVKEFLGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 QY 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120

DB 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 QY 181 PNVARNALVNCALVTVYDILKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 DB 181 PNVARNALVNCALVTVYDILKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYMNSALGOYSAGHCALITMLQKGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMNSALGOYSAGHCALITMLQKGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 3
 PCT-US99-06317-3
 Sequence 3, Application PC/TUS9906317
 GENERAL INFORMATION:
 APPLICANT: Garvey, W. Timothy
 APPLICANT: Argyropoulos, George
 TITLE OF INVENTION: METHODS FOR IDENTIFYING A RISK TO UCP2 AND UCP3
 TITLE OF INVENTION: GENE VARIANT-RELATED AFFILIATIONS AND COMPOSITIONS
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: 19113.0069/P
 CURRENT APPLICATION NUMBER: PCT/US99/06317
 CURRENT FILING DATE: 1999-03-23
 EARLIER APPLICATION NUMBER: 60/078,972
 EARLIER FILING DATE: 1998-03-23
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 3
 LENGTH: 309
 TYPE: PRT
 ORGANISM: Homo sapien
 FEATURE:
 OTHER INFORMATION: Note:/corresponds to human UCP2
 PCT-US99-06317-3

Query Match 100.0%; Score 1576; DB 1; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1.8e-159;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGFKATDVPPATATVKEFLGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 DB 1 MGGFKATDVPPATATVKEFLGAGTACIADLITFPDITAKVRLQIQESQGPVATASQYR 60
 QY 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 DB 61 GVMGTLTMVTEGPRSLYNGLVAGLORQMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
 QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 QY 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 DB 121 LAGSTTGALAAVAVAQPTDVVKVRFQOARAGGGRYQSTVNAKKTIAREEGFRGLMKGTS 180
 QY 181 PNVARNALVNCALVTVYDILKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 DB 181 PNVARNALVNCALVTVYDILKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVDVYKT 240
 QY 241 RYMNSALGOYSAGHCALITMLQKGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
 DB 241 RYMNSALGOYSAGHCALITMLQKGPRAFYKGFMPSPFLRLGSMNVVMFVTEQLKRALMA 300
 QY 301 ACTSREAPF 309
 DB 301 ACTSREAPF 309

RESULT 4

PCT-US99-17246-2
; Sequence 2, Application PC/TUS9917246
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-001100PC
; CURRENT APPLICATION NUMBER: PCT/US99/17246
; CURRENT FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: US 09/124,293
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-17246-2

Query Match 100.0%; Score 1576; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPATATVKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
DB 1 MVGFKATDVPPATATVKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
QY 61 GWMGTTILTWRTGPRSLYNGVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTTILTWRTGPRSLYNGVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIVNCAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVYVKT 240
DB 181 PNVARNAIVNCAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVYVKT 240
QY 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLSGSNVVMFVTEQLKRALMA 300
DB 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLSGSNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 5
US-09-012-218-1
; Sequence 1, Application US/09012218A
; GENERAL INFORMATION:
; APPLICANT: Picoult-Vioilik, Leslie
; TITLE OF INVENTION: Single Nucleotide Polymorphisms of the
; TITLE OF INVENTION: Uncoupling Protein 2 (UCP2) Gene
; FILE REFERENCE: 04990.0048
; CURRENT APPLICATION NUMBER: US/09/012,218A
; CURRENT FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-012-218-1

Query Match 100.0%; Score 1576; DB 14; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPATATVKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60

DB 1 MVGFKATDVPPATATVKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
QY 61 GWMGTTILTWRTGPRSLYNGVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTTILTWRTGPRSLYNGVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIVNCAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVYVKT 240
DB 181 PNVARNAIVNCAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVYVKT 240
QY 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLSGSNVVMFVTEQLKRALMA 300
DB 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLSGSNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 6
US-09-124-293-2
; Sequence 2, Application US/09124293
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, M. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 018781-001100
; CURRENT APPLICATION NUMBER: US/09/124,293
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-124-293-2

Query Match 100.0%; Score 1576; DB 15; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVGFKATDVPPATATVKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
DB 1 MVGFKATDVPPATATVKFLGAGTACIADLITFPDITAKVRLQIGESGQPVATASQYR 60
QY 61 GWMGTTILTWRTGPRSLYNGVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTTILTWRTGPRSLYNGVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LASTTGALAAVAAGTDPVVKRFOQARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIVNCAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVYVKT 240
DB 181 PNVARNAIVNCAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGCTTVIASPVYVKT 240
QY 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLSGSNVVMFVTEQLKRALMA 300
DB 241 RYNSALGQYSSAGHCALTMLOKEGPRAFYKGFMSFRLSGSNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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RESULT 7
US-09-277-575-8
/ Sequence 8, Application US/09277575
/ GENERAL INFORMATION:
/ APPLICANT: Newell, Martha K.
/ TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO
/ TITLE OF INVENTION: METABOLIC INTERACTIONS IN DISEASE
/ FILE REFERENCE: V0139/7028/HX
/ CURRENT APPLICATION NUMBER: US/09/277,575
/ CURRENT FILING DATE: 1999-03-26
/ EARLIER APPLICATION NUMBER: U.S. 60/082,250
/ EARLIER FILING DATE: 1998-04-17
/ EARLIER APPLICATION NUMBER: U.S. 60/094,519
/ EARLIER FILING DATE: 1998-07-29
/ EARLIER APPLICATION NUMBER: U.S. 60/101,580
/ EARLIER FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 309
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-277-575-8

Query Match          100.0%; Score 1576; DB 16; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFKATDVPTATVKEFGAGTAACIADLITFPLDTAKVRLQIGESQGPVATASAOYR 60
DB 1 MGFKATDVPTATVKEFGAGTAACIADLITFPLDTAKVRLQIGESQGPVATASAOYR 60
QY 61 GVMGTTILMTVRETEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVMGTTILMTVRETEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTGALAVAVAOPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTGALAVAVAOPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIVNCALVETVDLIKDALIKANLMTDDLPCHTSAFGAGCCTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCALVETVDLIKDALIKANLMTDDLPCHTSAFGAGCCTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGCHALTMLQKGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
DB 241 RYMNSALGOYSSAGCHALTMLQKGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 8
US-09-353-645-1
/ Sequence 1, Application US/09353645
/ GENERAL INFORMATION:
/ APPLICANT: SURWIT, RICHARD S.
/ APPLICANT: COLLINS, SHEILA A.
/ APPLICANT: WARDEN, CRAIG H.
/ APPLICANT: SELDIN, MICHAEL F.
/ APPLICANT: RICOUTER, DANIEL
/ APPLICANT: BOULLAUD, FREDERIC
/ TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
/ FILE REFERENCE: 1579-376
/ CURRENT APPLICATION NUMBER: US/09/353,645
/ CURRENT FILING DATE: 1999-07-15
/ PRIOR APPLICATION NUMBER: PCT/US97/06864
/ PRIOR FILING DATE: 1997-04-22
/ PRIOR APPLICATION NUMBER: 60/034,960
/ PRIOR FILING DATE: 1997-01-15
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: Patentin Ver. 2.1

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/ SEQ ID NO 1
/ LENGTH: 309
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-353-645-1

Query Match          100.0%; Score 1576; DB 17; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFKATDVPTATVKEFGAGTAACIADLITFPLDTAKVRLQIGESQGPVATASAOYR 60
DB 1 MGFKATDVPTATVKEFGAGTAACIADLITFPLDTAKVRLQIGESQGPVATASAOYR 60
QY 61 GVMGTTILMTVRETEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVMGTTILMTVRETEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTGALAVAVAOPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTGALAVAVAOPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIVNCALVETVDLIKDALIKANLMTDDLPCHTSAFGAGCCTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCALVETVDLIKDALIKANLMTDDLPCHTSAFGAGCCTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGCHALTMLQKGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
DB 241 RYMNSALGOYSSAGCHALTMLQKGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 9
US-09-433-622-34
/ Sequence 34, Application US/09433622A
/ GENERAL INFORMATION:
/ APPLICANT: Pan, James
/ APPLICANT: Adams, Sean
/ TITLE OF INVENTION: UCPS
/ FILE REFERENCE: P163R2
/ CURRENT APPLICATION NUMBER: US/09/433,622A
/ CURRENT FILING DATE: 1999-11-02
/ EARLIER APPLICATION NUMBER: US 60/110,286
/ EARLIER FILING DATE: 1998-11-30
/ EARLIER APPLICATION NUMBER: US 60/129,583
/ EARLIER FILING DATE: 1999-04-16
/ EARLIER APPLICATION NUMBER: US 60/143,886
/ EARLIER FILING DATE: 1999-07-15
/ NUMBER OF SEQ ID NOS: 36
/ SEQ ID NO 34
/ LENGTH: 309
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-433-622-34

Query Match          100.0%; Score 1576; DB 18; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFKATDVPTATVKEFGAGTAACIADLITFPLDTAKVRLQIGESQGPVATASAOYR 60
DB 1 MGFKATDVPTATVKEFGAGTAACIADLITFPLDTAKVRLQIGESQGPVATASAOYR 60
QY 61 GVMGTTILMTVRETEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GVMGTTILMTVRETEGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTGALAVAVAOPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTGALAVAVAOPTDVVKVRFQOARAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIVNCALVETVDLIKDALIKANLMTDDLPCHTSAFGAGCCTTVIASPVDVYKT 240
DB 181 PNVARNAIVNCALVETVDLIKDALIKANLMTDDLPCHTSAFGAGCCTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGCHALTMLQKGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
DB 241 RYMNSALGOYSSAGCHALTMLQKGPRAFYKGFMSFRLGSMNVVMFVTEQLKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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QY 181 PNVARNAINVCAELVTVYDLIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
181 PNVARNAINVCAELVTVYDLIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
QY 241 RYNNNSALGOYSSAGHCAITMLQKESGPRAFYKGMPSFLRSGMNVMMFVYEQLRALMA 300
241 RYNNNSALGOYSSAGHCAITMLQKESGPRAFYKGMPSFLRSGMNVMMFVYEQLRALMA 300
Db 301 ACTSREAPF 309
301 ACTSREAPF 309

RESULT 10
US-09-599-760-4
Sequence 4, Application US/09599760
GENERAL INFORMATION:
APPLICANT: Newell, Martha K.
TITLE OF INVENTION: Methods and Products for Manipulating
TITLE OF INVENTION: Uncoupling Protein Expression in the Plasma Membrane
FILE REFERENCE: 10277/7009
CURRENT APPLICATION NUMBER: US/09/599,760
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/140,574
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-599-760-4

Query Match 100.0%; Score 1576; DB 19; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPATATKFLGAGTAACIADLITPPLDTAKVRLQIQESGSPVRATASQYR 60
1 MNGFKATDVPPATATKFLGAGTAACIADLITPPLDTAKVRLQIQESGSPVRATASQYR 60
Db 61 GWMGTILTMVTEGPRSLYNGLVAGLQKQSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
61 GWMGTILTMVTEGPRSLYNGLVAGLQKQSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
QY 121 LAGSTGALAAVAAPPTDVYKVFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
121 LAGSTGALAAVAAPPTDVYKVFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
Db 181 PNVARNAINVCAELVTVYDLIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
181 PNVARNAINVCAELVTVYDLIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
QY 241 RYNNNSALGOYSSAGHCAITMLQKESGPRAFYKGMPSFLRSGMNVMMFVYEQLRALMA 300
241 RYNNNSALGOYSSAGHCAITMLQKESGPRAFYKGMPSFLRSGMNVMMFVYEQLRALMA 300
Db 301 ACTSREAPF 309
301 ACTSREAPF 309

RESULT 11
US-09-711-022-8
Sequence 8, Application US/09711022
GENERAL INFORMATION:
APPLICANT: MARTHA K. NEWELL
TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO
TITLE OF INVENTION: METABOLIC INTERACTIONS IN DISEASE
FILE REFERENCE: V0139/7028
CURRENT APPLICATION NUMBER: US/09/711,022
CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: U.S. 60/082,250
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: U.S. 60/094,519
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: U.S. 60/101,580
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 309
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-711-022-8

Query Match 100.0%; Score 1576; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPATATKFLGAGTAACIADLITPPLDTAKVRLQIQESGSPVRATASQYR 60
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Db 61 GWMGTILTMVTEGPRSLYNGLVAGLQKQSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
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QY 121 LAGSTGALAAVAAPPTDVYKVFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
121 LAGSTGALAAVAAPPTDVYKVFQOARAGGRRYOSTVNAKYTIAREEGFRGLMKGTS 180
Db 181 PNVARNAINVCAELVTVYDLIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
181 PNVARNAINVCAELVTVYDLIKDALLKANIMTDDLPCHEFTSAFGAGCTTVIASPVDVYKT 240
QY 241 RYNNNSALGOYSSAGHCAITMLQKESGPRAFYKGMPSFLRSGMNVMMFVYEQLRALMA 300
241 RYNNNSALGOYSSAGHCAITMLQKESGPRAFYKGMPSFLRSGMNVMMFVYEQLRALMA 300
Db 301 ACTSREAPF 309
301 ACTSREAPF 309

RESULT 12
US-09-711-022A-8
Sequence 8, Application US/09711022A
GENERAL INFORMATION:
APPLICANT: Newell, Martha K.
TITLE OF INVENTION: Methods and products related to metabolic interactions in di
FILE REFERENCE: V0139/7028
CURRENT APPLICATION NUMBER: US/09/711,022A
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/094,519
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: US 60/101,580
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-711-022A-8

Query Match 100.0%; Score 1576; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1,8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGFKATDVPPATATKFLGAGTAACIADLITPPLDTAKVRLQIQESGSPVRATASQYR 60
1 MNGFKATDVPPATATKFLGAGTAACIADLITPPLDTAKVRLQIQESGSPVRATASQYR 60
Db 61 GWMGTILTMVTEGPRSLYNGLVAGLQKQSPASVRIGLYDSVKQFTYKSGEHSISGRL 120
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Db      61 GWMGTLTLMVTEGPRSLYNGLVAGLQOMSFASVRLIGLVDSVQFTKSEHASIGSRL 120
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Db      121 LAGSTTGALAAVAAPPTDVVKVRFQAPARAGGRRYOSTVNAKYTIAREEGFGLMKGTS 180
Qy      181 PNVARNALVNCALVETVYDLIKDALIKALMTDDLPCHTSAFGAGCTTVIASPVVYKT 240
Db      181 PNVARNALVNCALVETVYDLIKDALIKALMTDDLPCHTSAFGAGCTTVIASPVVYKT 240
Qy      241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKRALMA 300
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Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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RESULT 13
US-09-743-847-4
; Sequence 4, Application US/09743847
; GENERAL INFORMATION:
; APPLICANT: Amylin Pharmaceuticals, Inc.
; APPLICANT: Albrandt, Keith
; APPLICANT: Beaumont, Kevin
; APPLICANT: Young, Andrew
; TITLE OF INVENTION: UNCOUPLIN PROTEIN 4 (UCP-4) AND METHODS OF USE
; FILE REFERENCE: 235/108 .0026
; CURRENT APPLICATION NUMBER: US/09/743,847
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/092,737
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: PCT/US99/15861
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-743-847-4

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Query Match      100.0%; Score 1576; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 GWMGTLTLMVTEGPRSLYNGLVAGLQOMSFASVRLIGLVDSVQFTKSEHASIGSRL 120
Db      61 GWMGTLTLMVTEGPRSLYNGLVAGLQOMSFASVRLIGLVDSVQFTKSEHASIGSRL 120
Qy      121 LAGSTTGALAAVAAPPTDVVKVRFQAPARAGGRRYOSTVNAKYTIAREEGFGLMKGTS 180
Db      121 LAGSTTGALAAVAAPPTDVVKVRFQAPARAGGRRYOSTVNAKYTIAREEGFGLMKGTS 180
Qy      181 PNVARNALVNCALVETVYDLIKDALIKALMTDDLPCHTSAFGAGCTTVIASPVVYKT 240
Db      181 PNVARNALVNCALVETVYDLIKDALIKALMTDDLPCHTSAFGAGCTTVIASPVVYKT 240
Qy      241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKRALMA 300
Db      241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKRALMA 300
Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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RESULT 14
US-09-884-814-1
; Sequence 1, Application US/09884814
; GENERAL INFORMATION:
; APPLICANT: Chen, Jin-Long
; APPLICANT: Amaral, W. Catherine
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Human Uncoupling Protein 2 (hUCP2): Compositions and
; FILE REFERENCE: 018781-001110US
; CURRENT APPLICATION NUMBER: US/09/884,814
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 09/124,293
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human uncoupling protein 2 (hUCP2) Chen (Tularik)
; US-09-884-814-1

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Query Match      100.0%; Score 1576; DB 23; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e-159;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MVEFKATDVPTATVVKFLGAGTAACIADLITPPLDTAKVRLQIGESQGPVATASAOYR 60
Qy      61 GWMGTLTLMVTEGPRSLYNGLVAGLQOMSFASVRLIGLVDSVQFTKSEHASIGSRL 120
Db      61 GWMGTLTLMVTEGPRSLYNGLVAGLQOMSFASVRLIGLVDSVQFTKSEHASIGSRL 120
Qy      121 LAGSTTGALAAVAAPPTDVVKVRFQAPARAGGRRYOSTVNAKYTIAREEGFGLMKGTS 180
Db      121 LAGSTTGALAAVAAPPTDVVKVRFQAPARAGGRRYOSTVNAKYTIAREEGFGLMKGTS 180
Qy      181 PNVARNALVNCALVETVYDLIKDALIKALMTDDLPCHTSAFGAGCTTVIASPVVYKT 240
Db      181 PNVARNALVNCALVETVYDLIKDALIKALMTDDLPCHTSAFGAGCTTVIASPVVYKT 240
Qy      241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKRALMA 300
Db      241 RYNSALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLRGSNNVVMFVTEQLKRALMA 300
Qy      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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RESULT 15
US-10-265-689-1
; Sequence 1, Application US/10265689
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOUTILAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15

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; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 309
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-265-689-1

Query Match 100.0%; Score 1576; DB 28; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1,8e-159;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MVGFKATDVPPPTATVFLGAGTACTADLITFPPLDTAKVRLQIQGHSQGPVATASAQYR	60
QY	61	GVMGTTITMVRTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYTKGSEHASIGSRL	120
DB	61	GVMGTTITMVRTEGPRSLYNGLVAGLQRCMSFASVRIGLYDSVKQFYTKGSEHASIGSRL	120
QY	121	LASSTGALAVAAQPTDVVKVRFQQAQARAGGRRYQSTYNAYKTIAREEGFRGLMKGTS	180
DB	121	LASSTGALAVAAQPTDVVKVRFQQAQARAGGRRYQSTYNAYKTIAREEGFRGLMKGTS	180
QY	181	PNVARNALVNCALVTVTDLIKDALKANLMTDDLPGHFTSAFGAGFCTVIASPDVYKTI	240
DB	181	PNVARNALVNCALVTVTDLIKDALKANLMTDDLPGHFTSAFGAGFCTVIASPDVYKTI	240
QY	241	RYMNSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRIGSNVVMFVTTYEQLKALMA	300
DB	241	RYMNSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSEFLRIGSNVVMFVTTYEQLKALMA	300
QY	301	ACTSREAPF 309	
DB	301	ACTSREAPF 309	

Search completed: February 4, 2004, 09:23:37
 Job time : 176 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 4, 2004, 09:18:34 ; Search time 23 Seconds
(without alignments)
1045,650 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576

Sequence: 1 MGFKATDVPPTATVKFLGA.....TYEQKRALMAACTSRAPF 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 376054 seqs, 77831530 residues

Total number of hits satisfying chosen parameters: 376054

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA.New.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1576	100.0	309	US-09-599-760B-4	Sequence 4, Appli
2	1576	100.0	309	US-10-671-628-8	Sequence 8, Appli
3	1576	100.0	309	US-10-616-865-8	Sequence 8, Appli
4	1576	100.0	309	US-60-485-450-1467	Sequence 1467, Ap
5	1496	94.9	309	US-10-743-643-170	Sequence 170, App
6	1496	94.9	309	US-60-531-341-501	Sequence 501, App
7	1149.5	72.9	312	US-10-671-628-9	Sequence 9, Appli
8	1149.5	72.9	312	US-60-490-890-852	Sequence 852, App
9	998.5	63.4	275	US-09-599-760B-6	Sequence 6, Appli
10	998.5	63.4	275	US-10-616-865-10	Sequence 10, Appli
11	998.5	63.4	275	US-10-743-643-172	Sequence 172, App
12	998.5	63.4	275	US-60-490-890-854	Sequence 854, App
13	998.5	63.4	275	US-60-531-341-503	Sequence 503, App
14	915	58.1	307	US-09-599-760B-2	Sequence 2, Appli
15	915	58.1	307	US-10-616-865-6	Sequence 6, Appli
16	907	57.6	307	US-10-671-628-7	Sequence 7, Appli
17	693	44.0	345	US-10-425-114A-66317	Sequence 66317, A
18	674.5	42.8	303	US-10-671-628-2	Sequence 2, Appli
19	671.5	42.1	306	US-10-671-628-5	Sequence 5, Appli
20	663.5	42.1	306	US-10-671-628-6	Sequence 6, Appli
21	594	37.7	268	US-10-671-628-4	Sequence 4, Appli
22	495	31.4	340	US-09-614-150A-14019	Sequence 14019, A
23	492.5	31.2	341	US-10-425-114A-52234	Sequence 52234, A
24	479.5	30.4	303	US-09-614-150A-16338	Sequence 16338, A
25	455.5	28.9	330	US-10-739-330-6246	Sequence 6246, Ap
26	441.5	28.0	336	PCT-US03-28227-4124	Sequence 4124, Ap

27	436.5	27.7	329	US-10-258-899A-1936	Sequence 1936, Ap
28	420.5	26.7	337	US-09-614-150A-27447	Sequence 27447, A
29	416.5	26.4	314	US-10-743-643-1602	Sequence 1602, Ap
30	416.5	26.4	314	US-60-531-341-1432	Sequence 1432, Ap
31	411.5	26.1	314	US-10-743-643-1604	Sequence 1604, Ap
32	411.5	26.1	314	US-60-531-341-1434	Sequence 1434, Ap
33	408	25.9	312	US-10-425-114A-59754	Sequence 59754, A
34	408	25.9	335	US-09-614-150A-19419	Sequence 19419, A
35	403	25.6	335	US-10-432-737-5	Sequence 5, Appli
36	400	25.4	317	US-09-614-150A-815	Sequence 815, Appli
37	389	24.7	311	US-09-614-150A-27690	Sequence 27690, A
38	387.5	24.6	342	PCT-US03-24164-45	Sequence 45, Appli
39	370	23.5	280	US-09-614-150A-24396	Sequence 24396, A
40	370	23.5	280	US-09-614-150A-41871	Sequence 41871, A
41	367.5	23.3	301	US-09-614-150A-555	Sequence 555, App
42	360.5	22.9	287	US-09-614-150A-23403	Sequence 23403, A
43	349	22.1	296	US-09-614-150A-8460	Sequence 8460, Ap
44	345	21.9	302	US-09-614-150A-27507	Sequence 27507, A
45	340	21.6	263	PCT-US03-24164-36	Sequence 36, Appli

ALIGNMENTS

RESULT 1
US-09-599-760B-4
Sequence 4, Application US/09599760B
GENERAL INFORMATION:
APPLICANT: Newell, Martha K
TITLE OF INVENTION: Methods and products for manipulating uncoupling protein
FILE REFERENCE: V00139, 70059, US
CURRENT APPLICATION NUMBER: US/09/599, 760B
CURRENT FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/140,574
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-599-760B-4

Query Match 100.0%; Score 1576; DB 5; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGFKATDVPPTATVKFLGAGTAACTIDLTTFPLDTAKVRLQIGESQGPVATASAOYR	60
DB	1	MGFKATDVPPTATVKFLGAGTAACTIDLTTFPLDTAKVRLQIGESQGPVATASAOYR	60
QY	61	GWGCTILTWREGRSLYNGIVAGLQOMSFASVRIGLYSVQOFTKSEHASIGSRL	120
DB	61	GWGCTILTWREGRSLYNGIVAGLQOMSFASVRIGLYSVQOFTKSEHASIGSRL	120
QY	121	LAGSTTGALAVVAQPTVVVKRFQACRAGGRYSOTVNAVYKTIARESGFRGMKGS	180
DB	121	LAGSTTGALAVVAQPTVVVKRFQACRAGGRYSOTVNAVYKTIARESGFRGMKGS	180
QY	181	PVNAARNAVNCALVETTYLIDKALIKANIMTDDLPCHFTSAFGAGFCTTYIASVVDVKT	240
DB	181	PVNAARNAVNCALVETTYLIDKALIKANIMTDDLPCHFTSAFGAGFCTTYIASVVDVKT	240
QY	241	RYVNSALGGVSSAGCAITMLQKSGPRAFYKGPSPFLRLGSNAVVMETVYEQKRALMA	300
DB	241	RYVNSALGGVSSAGCAITMLQKSGPRAFYKGPSPFLRLGSNAVVMETVYEQKRALMA	300
QY	301	ACTSRAPF 309	
DB	301	ACTSRAPF 309	


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RESULT 2
US-10-671-628-8
; ORGANISM: Homo sapiens
; Sequence 8, Application US/10671628
; GENERAL INFORMATION:
; APPLICANT: ITO, Kikatsu
; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
; FILE REFERENCE: 2003-13864/WMC/00653
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 10/009,962
; PRIOR FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: PCT/JP00/03806
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: JP11-167439
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-628-8

Query Match      100.0%; Score 1576; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MWGFKATVPPTATVKEFLGAGTACIADLITFPDITAKVRLQIGESQGPVATASAYR 60
QY 61 GWMGTLITMVRTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLITMVRTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAVAAQPTDVVYKRFQAPRAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAQPTDVVYKRFQAPRAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
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DB 181 PNVARNAIYVNCALVETVDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
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DB 301 ACTSREAPF 309

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-865-8

Query Match      100.0%; Score 1576; DB 6; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGFKATVPPTATVKEFLGAGTACIADLITFPDITAKVRLQIGESQGPVATASAYR 60
DB 1 MWGFKATVPPTATVKEFLGAGTACIADLITFPDITAKVRLQIGESQGPVATASAYR 60
QY 61 GWMGTLITMVRTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLITMVRTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAVAAQPTDVVYKRFQAPRAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAQPTDVVYKRFQAPRAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIYVNCALVETVDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVDVYKT 240
DB 181 PNVARNAIYVNCALVETVDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

RESULT 4
US-60-485-450-1467
; Sequence 1467, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CHANG, Sheng-xiang
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
; TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
; FILE REFERENCE: C1001470
; CURRENT APPLICATION NUMBER: US/60/485,450
; NUMBER OF SEQ ID NOS: 47859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1467
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-485-450-1467

Query Match      100.0%; Score 1576; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.6e-150;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGFKATVPPTATVKEFLGAGTACIADLITFPDITAKVRLQIGESQGPVATASAYR 60
DB 1 MWGFKATVPPTATVKEFLGAGTACIADLITFPDITAKVRLQIGESQGPVATASAYR 60
QY 61 GWMGTLITMVRTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
DB 61 GWMGTLITMVRTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRL 120
QY 121 LAGSTTGALAVAAQPTDVVYKRFQAPRAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
DB 121 LAGSTTGALAVAAQPTDVVYKRFQAPRAGGRRYQSTVNAKYTIAREEGFRGLMKGTS 180
QY 181 PNVARNAIYVNCALVETVDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVDVYKT 240
DB 181 PNVARNAIYVNCALVETVDLIKDALIKANIMTDDLPCHTSAFGAGFCTTVIASPVDVYKT 240
QY 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
DB 241 RYMNSALGOYSSAGHCALTMLOKEGPRAFYKGFMSFRLISNNVVMFTYEQIKRALMA 300
QY 301 ACTSREAPF 309
DB 301 ACTSREAPF 309

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us-09-884-814-1.ram

Page 3

Qy	24	RYNNSALGQYSSAGHCLTMTLQEGPRAFYKGMPSFLTSGMNVYMEVTEQLRALMA	300
Db	241	RYNNSALGQYSSAGHCLTMTLQEGPRAFYKGMPSFLTSGMNVYMEVTEQLRALMA	300
Qy	301	ACTSREAP	309
Db	301	ACTSREAP	309

```

RESULT 5
US-10-743-643-170
; Sequence 170: Application US//10743643
; GENERAL INFORMATION:
; APPLICANT: Woolt et al.
; TITLE OF INVENTION: Nucleic acid and amino acid sequences involved in pain
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US//10/743,643
; CURRENT FILING DATE: 2003-12-22
; FILE REFERENCE:
; PRIOR APPLICATION NUMBER: 17633/2005
; PRIOR FILING DATE: 2003-12-22
; PRIOR FILING DATE: 2002/07/14
; NUMBER OF SEQ ID NOS: 2605
; SOFTWARE: Perl script
; SEQ ID NO 170
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; DATABASE ACCESSION NUMBER: Refseq / NP_062227
; DATABASE ENTRY DATE: 2003-01-13
US-10-743-643-170

```

Query Match	94.9%;	Score 1496;	DB 6;	Length 309;
Best Local Similarity	95.1%;	Pred. No. 2.8e-142;		
Matches 294; Conservative			Mismatches 13;	Indels 0; Gaps 0;

Qy	1	MVGRKADVPEPTAIYVKELAGTAIAACIADIITPELDTAKRLOIQEESGVPYATASQYR	60
Db	1	MVGRKADVPEPTAIYVKELAGTAIAACIADIITPELDTAKRLOIQEESGVLARTASQYR	60
Qy	61	GVWGVTILMTBTGPRESLNGLVAGIQROMSPASVRIGLYDSVKQFYTKGSEHASISRL	120
Db	61	GVLTGVTILMTBTGPRESLNGLVAGIQROMSPASVRIGLYDSVKQFYTKGSEHAIGISRL	120
Qy	121	LASGTGTLAAVAVAQPTDVKYKRFQAPADAGGGRPGYSIVNAYKTIIAEESFRLMGTS	180
Db	121	LASGTGTLAAVAVAQPTDVKYKRFQAPADAGGGRPGYVEAYKTIIAEESIRGLMGTS	180
Qy	181	PNVARNATVNCALVYTDLIKDALILKANLMTDDLPHFTSAGDAFCCTTVIASPVDVKT	240
Db	181	PNVARNATVNCETLVYTDLIKDTLLKANLMTDDLPHFTSAGDAFCCTTVIASPVDVKT	240
Qy	241	RYNMSALGQYSASGHCALTMLQKEGFPAPYKGFMSFIRLGSNNVMFVITYEQLKRALMA	300
Db	241	RYNMSALGQYHSAGHCALTMLRKEGPPTFYKGFMSFIRLGSNNVMFVITYEQLKRALMA	300
Qy	301	ACTSRAPF 309	
Db	301	AYESREAPF 309	

```

RESULT 6
US-60-531,341-501
; Sequence 501: Application US/60531341
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2041
; CURRENT APPLICATION NOS: US/60/531,341
; CURRENT FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script

```

```

; SEQ ID NO 501
;
; LENGTH: 309
;
; TYPE: PRT
;
; ORGANISM: Rattus norvegicus
;
; PUBLICATION INFORMATION:
;
; DATABASE ACCESSION NUMBER: Refseq / NP_062227
;
; DATABASE ENTRY DATE: 2003-10-05
;
US-60-531-341-501

```

Query Match	94.9%	Score 1496	DB 7	Length 309
Best Local Similarity	95.1%	Pred. No. 2.8e-142		
Matches 294	Conservative 2	Mismatches 13	Indels 0	Gaps 0

QY	1	MSEFKATDVEPRATVYFELDAGTAACIADLIIFPELDTAKVRLOIQGSEOGVRRATAOYR	60
Db	1	MSEFKATDVEPRATVYFELDAGTAACIADLIIFPELDTAKVRLOIQGSEOGVRRATAOYR	60
QY	61	GVNGTILTMWRTEGPRSLYNGVALQROMPSASVRIGLVDSVOQFTKSEHASTGSL	120
Db	61	GVNGTILTMWRTEGPRSLYNGVALQROMPSASVRIGLVDSVOQFTKSEHASTGSLR	120
QY	121	LAGSTTGALAVAAVACPTDVVKYRFQQAARAGGGRRYOSTVNAVYKTIARDEGFGMLKGTIS	180
Db	121	LAGSTTGALAVAAVACPTDVVKYRFQQAARAGGGRRYOSTVNAVYKTIARDEGFGMLKGTIS	180
QY	181	PNTARNAIVNCAJLVYTDILKALAKAMIMDDLPCHFTSAFGAGFCTVYIASPVVYKI	240
Db	181	PNTARNAIVNCAJLVYTDILKALAKAMIMDDLPCHFTSAFGAGFCTVYIASPVVYKI	240
QY	241	RYMNSALGOYSSAGHCAITMLQKEGPRAFYKGFMPFRLGSMNVNMFVYEEQLKRALMA	300
Db	241	RYMNSALGOYSSAGHCAITMLQKEGPRAFYKGFMPFRLGSMNVNMFVYEEQLKRALMA	300
QY	301	ACTSRREAPF 309	
Db	301	AYESREAPF 309	

```

      RESULT 7
      US-10-671-628-9
      ; Sequence 9, Application US/10671628
      ; GENERAL INFORMATION:
      ; APPLICANT: ITO, KIKUKATSU
      ; TITLE OF INVENTION: Plant Thermogenic Genes and Proteins
      ; FILE REFERENCE: 2003-13864/WG/00653
      ; CURRENT APPLICATION NUMBER: US/10/671,628
      ; CURRENT FILING DATE: 2003-09-29
      ; PRIOR APPLICATION NUMBER: 10/009,962
      ; PRIOR FILING DATE: 2002-01-23
      ; PRIOR APPLICATION NUMBER: PCT/JP00/03806
      ; PRIOR FILING DATE: 2000-06-12
      ; PRIOR APPLICATION NUMBER: JP1-167439
      ; PRIOR FILING DATE: 1999-06-14
      ; NUMBER OF SEQ ID NOS: 12
      ; SOFTWARE: PatentIn Ver. 2.0
      ; SEQ ID NO 9
      ;
      ; LENGTH: 312
      ;
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ;
      ; US-10-671-628-9

```

Query Match 72.9%; Score 1149.5; DB 6; Length 312;
Best Local Similarity 72.2%; Pred. No. 1.9e-107;
Matches 226; Conservative 31; Mismatches 51; Gaps 3

QY 1 MYGKRAIDVPELTIVKVLGAGTACIADIITPELTATKVR.LCIOESGCPAPATASAKYR 60
Db 1 MYGLKPSDVPTTAKVR.LGAGTACCPADLTPELTATKVR.LCIOENQA.VQTRALVQYR 59
QY 61 GVMGILTMVTFBSPSLINGVLVAGIQOMSTASVRLGIDYSVKQFYT.KSEHASIGSR 119
Db 60 GVLGILITLMTTEPCSPYINGVLVAGIQOMSPFSITIGIDYBKVQYVPFKADNSLTLR 118

```

QY 120 LLAGSTTGALAAVAAQPTDVYKVFQQAQABAG--GGRYQSTVNAKTIAREEGRGLW 176
DB 120 ILACCTTGAMAAVTCQAQPTDVYKVFQASIHGSRSDRKSGTMDARTTAREEGRGLW 179
QY 177 KGTSPNVARNAIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVTIASPYD 236
DB 180 KGTLPNIMRNAIVNCAELVTVYDLIKELLDYHLLTDNFPCHFVSARFAGFCAIVVASPYD 239
QY 237 VKTRRYNSALGOYSSAGHCALTMLOKEGPRAFYKGMBSFRLGSMNVMTPTTYEQLR 296
DB 240 VKTRRYNSPPGOYFSPDLCMIKVAQEGPTAFYKGPSPSFLRLGSMNVMTPTTYEQLR 299
QY 297 ALMAACTSREAPF 309
DB 300 ALMKVQMLRESPF 312

```

```

RESULT 8
US-60-490-890-852
; Sequence 852, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Kuprow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D03:0 PSP
; CURRENT APPLICATION NUMBER: US/60-490-890
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 852
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-852

```

```

Query Match 72.9%; Score 1149.5; DB 7; Length 312;
Best Local Similarity 72.2%; Pred. No. 1.9e-107;
Matches 226; Conservative 31; Mismatches 51; Indels 5; Gaps 3;

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```

QY 1 MGGFKATDVPEPTATVFLGAGTAACIADLTITPPLDTAKVRLQIQESQGPVATASQYR 60
DB 1 MGLKPSDVPPTMAVFKFJGAGTAACFADLVTFPLDTAKVRLQIQENQA-VQTRALVQYR 59
QY 61 GVGSTILTWRTGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
DB 60 GVLGTLTWRTGPRSPYNGLVAGLQROMSFASIRIGLYDSVKQVTPKQADNSLITR 119
QY 120 LLAGSTTGALAAVAAQPTDVYKVFQQAQABAG--GGRYQSTVNAKTIAREEGRGLW 176
DB 120 ILACCTTGAMAAVTCQAQPTDVYKVFQASIHGSRSDRKSGTMDARTTAREEGRGLW 179
QY 177 KGTSPNVARNAIVNCAELVTVYDLIKDALIKANIMTDDLPCHEFTSARFAGFCTVTIASPYD 236
DB 180 KGTLPNIMRNAIVNCAELVTVYDLIKELLDYHLLTDNFPCHFVSARFAGFCAIVVASPYD 239
QY 237 VKTRRYNSALGOYSSAGHCALTMLOKEGPRAFYKGMBSFRLGSMNVMTPTTYEQLR 296
DB 240 VKTRRYNSPPGOYFSPDLCMIKVAQEGPTAFYKGPSPSFLRLGSMNVMTPTTYEQLR 299
QY 297 ALMAACTSREAPF 309
DB 300 ALMKVQMLRESPF 312

```

```

RESULT 9
US-09-599-760B-6
; Sequence 6, Application US/09599760B
; GENERAL INFORMATION:
; APPLICANT: Newell, Martha K
; TITLE OF INVENTION: Methods and products for manipulating uncoupling protein

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; TITLE OF INVENTION: expression
; FILE REFERENCE: Y00139, 70059, US
; CURRENT APPLICATION NUMBER: US/09/599, 760B
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/140, 574
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-599-760B-6

```

```

Query Match 63.4%; Score 998.5; DB 5; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

```

```

RESULT 10
US-10-616-865-10
; Sequence 10, Application US/10616865
; GENERAL INFORMATION:
; APPLICANT: NEWELL, MARTHA K
; TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN D
; FILE REFERENCE: Y0139, 70017US00
; CURRENT APPLICATION NUMBER: US/10/616, 865
; CURRENT FILING DATE: 2003-07-05
; PRIOR APPLICATION NUMBER: US 09/277, 575
; PRIOR FILING DATE: 1999-03-27
; PRIOR APPLICATION NUMBER: US 60/082, 250
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/101, 580
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: US 60/094, 519
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-865-10

```

```

Query Match 63.4%; Score 998.5; DB 6; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

```

```

Db      60 GVLGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
        120 LLAGSTTGALAVAAQPTDVVKVRFQAQARAG---GGRRYSTNAKYKTIAEEGFRGLW 176
        120 ILAGCTTGAMAAVTCAPPTDVVKVRFQASIHLPSPSDRKYSGTMDAYRTIAREEGVGLW 179
Qy      177 KGTSPVANAIAVNCALVETVDLIDKALLKANIMTDDLPCHEFTSAFGAGFCTTVIASPVD 236
        180 KGTLPNIMENAIVNCAEVVTVYDILKEKLLDHLITDNPCHFSVAFGAGFCATVVASPVD 239
Db      237 VVKTRYMNSALQYSSAGHCALTMLOKEGPRAFYKG 272
        240 VVKTRYMNSPPGQYFSPPLDCMIMVAQEGPTAFYKG 275

```

RESULT 11

```

US-10-743-643-172
; Sequence 172, Application US/10743643
; GENERAL INFORMATION:
; APPLICANT: Woolf et al.
; TITLE OF INVENTION: Nucleic acid and amino acid sequences involved in pain
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/743,643
; PRIORITY FILING DATE: 2003-12-22
; FILE REFERENCE: 17633/2005
; PRIORITY APPLICATION NUMBER: 10/219,051
; PRIORITY FILING DATE: 2002/07/14
; NUMBER OF SEQ ID NOS: 2605
; SOFTWARE: Perl script
; SEQ ID NO 172
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; DATABASE ACCESSION NUMBER: Refseq / NP_073714
; DATABASE ENTRY DATE: 2001-03-09
US-10-743-643-172

```

```

Query Match      63.4%; Score 998.5; DB 6; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

```

```

Qy      1 MVGPKATDVPPATVVKFLGAGTACIADLITFPLDTAKVRLQIQESGQPVATASQYR 60
        1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTFPLDTAKVRLQIQENQA-VQTAALVQYR 59
Db      61 GVMGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
        60 GVLGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
Qy      120 LLAGSTTGALAVAAQPTDVVKVRFQAQARAG---GGRRYSTNAKYKTIAEEGFRGLW 176
        120 ILAGCTTGAMAAVTCAPPTDVVKVRFQASIHLPSPSDRKYSGTMDAYRTIAREEGVGLW 179
Db      177 KGTSPVANAIAVNCALVETVDLIDKALLKANIMTDDLPCHEFTSAFGAGFCTTVIASPVD 236
        180 KGTLPNIMENAIVNCAEVVTVYDILKEKLLDHLITDNPCHFSVAFGAGFCATVVASPVD 239
Qy      237 VVKTRYMNSALQYSSAGHCALTMLOKEGPRAFYKG 272
        240 VVKTRYMNSPPGQYFSPPLDCMIMVAQEGPTAFYKG 275

```

RESULT 12

```

US-60-490-890-854
; Sequence 854, Application US/60490890
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION

```

```

; FILE REFERENCE: D0310 PSP
; CURRENT APPLICATION NUMBER: US/60/490,890
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2779
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 854
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-490-890-854

```

```

Query Match      63.4%; Score 998.5; DB 7; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

```

```

Qy      1 MVGPKATDVPPATVVKFLGAGTACIADLITFPLDTAKVRLQIQESGQPVATASQYR 60
        1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTFPLDTAKVRLQIQENQA-VQTAALVQYR 59
Db      61 GVMGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
        60 GVLGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
Qy      120 LLAGSTTGALAVAAQPTDVVKVRFQAQARAG---GGRRYSTNAKYKTIAEEGFRGLW 176
        120 ILAGCTTGAMAAVTCAPPTDVVKVRFQASIHLPSPSDRKYSGTMDAYRTIAREEGVGLW 179
Db      177 KGTSPVANAIAVNCALVETVDLIDKALLKANIMTDDLPCHEFTSAFGAGFCTTVIASPVD 236
        180 KGTLPNIMENAIVNCAEVVTVYDILKEKLLDHLITDNPCHFSVAFGAGFCATVVASPVD 239
Qy      237 VVKTRYMNSALQYSSAGHCALTMLOKEGPRAFYKG 272
        240 VVKTRYMNSPPGQYFSPPLDCMIMVAQEGPTAFYKG 275

```

RESULT 13

```

US-60-531-341-503
; Sequence 503, Application US/60531341
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts Gene
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: 17633/2041
; CURRENT APPLICATION NUMBER: US/60/531,341
; PRIORITY FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 2587
; SOFTWARE: Perl script
; SEQ ID NO 503
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_073714
; DATABASE ENTRY DATE: 2003-10-05
US-60-531-341-503

```

```

Query Match      63.4%; Score 998.5; DB 7; Length 275;
Best Local Similarity 71.0%; Pred. No. 2.4e-92;
Matches 196; Conservative 30; Mismatches 45; Indels 5; Gaps 3;

```

```

Qy      1 MVGPKATDVPPATVVKFLGAGTACIADLITFPLDTAKVRLQIQESGQPVATASQYR 60
        1 MVGLKPSDVPPTMAVKFLGAGTACFADLVTFPLDTAKVRLQIQENQA-VQTAALVQYR 59
Db      61 GVMGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
        60 GVLGTLTWMRTGEGSPYNGLVAGLQROMSFASIRILYDSVKQVTPPKADNSLITR 119
Qy      120 LLAGSTTGALAVAAQPTDVVKVRFQAQARAG---GGRRYSTNAKYKTIAEEGFRGLW 176
        120 ILAGCTTGAMAAVTCAPPTDVVKVRFQASIHLPSPSDRKYSGTMDAYRTIAREEGVGLW 179

```

```

QY 177 KGISPNVARNALVNCALVYDILKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPD 236
DB 180 KGLTFNIMRNALVNCALVYDILKDALIKANIMTDDLPCHFTSAGAGCAIVASPD 239
QY 237 VKTRYNSALGOYSSAGHCHALTMLOKEGPRAPFYK 272
DB 240 VKTRYNSPPGOYSSAGHCHALTMLOKEGPRAPFYK 275

```

RESULT 14

```

US-09-599-760B-2
Sequence 2, Application US/09599760B
GENERAL INFORMATION:
APPLICANT: Newell, Martha K
TITLE OF INVENTION: Methods and products for manipulating uncoupling protein
FILE REFERENCE: V00139.70059.US
CURRENT APPLICATION NUMBER: US/09/599.760B
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/140,574
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 307
TYPE: PRT
ORGANISM: Homo sapiens
US-09-599-760B-2

```

```

Query Match 58.1%; Score 915; DB 5; Length 307;
Best Local Similarity 59.3%; Pred. No. 6,7e-84;
Matches 178; Conservative 48; Mismatches 68; Indels 6; Gaps 3;

```

```

QY 1 MGCFKATDVPPNATVYKFLAGAGTACIADITPPDITAKYRLQIOGESGQPVATASQYR 60
DB 1 MGGLTASDVHPTLGVQLFSAGIAACIADVITPPDITAKYRLQVQGECP---TSSVIRYK 56
QY 61 GVMGTLITVWTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFTYKSEHA-SIGSR 119
DB 57 GVLGTTAVVKTEGRKLYSGLPAGLQRISSASRLIGLYDVQEFITAGKETAPSLGSK 116
QY 120 LLAGSTTGALAVVAQPTDVYKVRFOAQRAGGR-RYOSTVNAKYTIAREGFRGLMKG 178
DB 117 ILAGLTGGVAVFIGQPTDEVKVRLOAQSHLGIKRYGTYNAYRIIATTEGLTGLMKG 176
QY 179 TSPNVARNALVNCALVYDILKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPDVY 238
DB 177 TTPNLMRSVLIINCTELVYDILKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPDVY 236
QY 239 KTRYNSALGOYSSAGHCHALTMLOKEGPRAPFYKGMPSFLRLGSMNVVMFTYEQLRAL 298
DB 237 KTRFINSPPGOYSSAGHCHALTMLOKEGPRAPFYKGMPSFLRLGSMNVVMFTYEQLRAL 296

```

RESULT 15

```

US-10-616-865-6
Sequence 6, Application US/10616865
GENERAL INFORMATION:
APPLICANT: NEWELL, MARTHA K
TITLE OF INVENTION: METHODS AND PRODUCTS RELATED TO METABOLIC INTERACTIONS IN DISEASE
FILE REFERENCE: V0139.70017US00
CURRENT APPLICATION NUMBER: US/10/616,865
PRIOR FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 09/277,575
PRIOR FILING DATE: 1999-03-27
PRIOR APPLICATION NUMBER: US 60/082,250
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/101,580
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 60/094,519
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 6
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-865-6

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Query Match 58.1%; Score 915; DB 6; Length 307;
Best Local Similarity 59.3%; Pred. No. 6,7e-84;
Matches 178; Conservative 48; Mismatches 68; Indels 6; Gaps 3;

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QY 1 MGCFKATDVPPNATVYKFLAGAGTACIADITPPDITAKYRLQIOGESGQPVATASQYR 60
DB 1 MGGLTASDVHPTLGVQLFSAGIAACIADVITPPDITAKYRLQVQGECP---TSSVIRYK 56
QY 61 GVMGTLITVWTEGPRSLYNGVLVAGLQROMSPASVRIGLYDSVKQFTYKSEHA-SIGSR 119
DB 57 GVLGTTAVVKTEGRKLYSGLPAGLQRISSASRLIGLYDVQEFITAGKETAPSLGSK 116
QY 120 LLAGSTTGALAVVAQPTDVYKVRFOAQRAGGR-RYOSTVNAKYTIAREGFRGLMKG 178
DB 117 ILAGLTGGVAVFIGQPTDEVKVRLOAQSHLGIKRYGTYNAYRIIATTEGLTGLMKG 176
QY 179 TSPNVARNALVNCALVYDILKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPDVY 238
DB 177 TTPNLMRSVLIINCTELVYDILKDALIKANIMTDDLPCHFTSAGAGCTTIVIASPDVY 236
QY 239 KTRYNSALGOYSSAGHCHALTMLOKEGPRAPFYKGMPSFLRLGSMNVVMFTYEQLRAL 298
DB 237 KTRFINSPPGOYSSAGHCHALTMLOKEGPRAPFYKGMPSFLRLGSMNVVMFTYEQLRAL 296

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Search completed: February 4, 2004, 09:24:12
Job time : 24 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 09:16:38 ; Search time 21 Seconds
(without alignments)

1415.053 Million cell updates/sec

Title: US-09-884-814-1
Perfect score: 1576
Sequence: 1 MVGFKATDVPPTATVFLGA.....TYEQKRALMDACTSREAPF 309

Scoring table: BUCSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	DB	ID	Description
1	1149.5	72.9	312	2	JC5522	uncoupling protein
2	959.5	60.9	306	2	A32446	uncoupling protein
3	928.5	58.9	307	2	A26294	uncoupling protein
4	915.5	58.1	307	2	S34268	uncoupling protein
5	915	58.1	307	2	G01858	uncoupling protein
6	911.5	57.8	306	2	A31106	mitochondrial unco
7	907.5	57.6	288	2	S03603	uncoupling protein
8	693.5	44.0	306	2	T47570	uncoupling protein
9	684.5	43.4	306	2	T52024	uncoupling protein
10	671.5	42.6	306	2	T07793	uncoupling protein
11	520.5	33.0	325	2	UC7553	brain mitochondria
12	483.5	30.7	313	2	T05577	uncoupling protein
13	475.5	30.2	313	2	D84613	uncoupling prote
14	466	29.6	305	2	H86274	hypothetical prote
15	446.5	28.3	323	2	T35459	hypothetical prote
16	415.5	26.4	314	2	A36305	2-oxoglutarate/mal
17	413	26.2	282	2	T49628	probable dicarboxy
18	411.5	26.1	314	2	A56650	2-oxoglutarate car
19	398.5	25.3	343	2	T15253	hypothetical prote
20	379.5	24.1	290	2	S44091	oxoglutarate/malat
21	360	22.8	298	2	S51351	hypothetical prote
22	339.5	21.5	324	2	S25357	mitochondrial unco
23	307	19.5	302	2	S65042	2-oxoglutarate/mal
24	307	19.5	302	2	S65040	2-oxoglutarate/mal
25	297.5	18.3	331	2	T51899	probable 2-oxogluc
26	292.5	18.6	297	2	S57116	probable carrier p
27	277.5	17.6	93	2	T07405	oxoglutarate/malat
28	273	17.3	311	2	S16082	uncoupling protein
29					G01789	citrate transpor

30	273	17.3	311	2	A46595	tricarboxylate tra
31	263.5	16.7	309	2	T48156	hypothetical prote
32	260.5	16.5	352	2	T01729	mitochondrial solu
33	256.5	16.3	447	2	T00435	probable mitochond
34	255.5	16.2	298	2	B43646	ADP ATP carrier pr
35	255.5	16.2	302	2	T38879	probable mitochond
36	254.5	16.1	298	1	S03894	ADP ATP carrier pr
37	254.5	16.1	299	2	S44554	citrate transport
38	254.5	16.1	358	2	T09109	envelope protein L
39	253.5	16.1	358	1	XWBO	ADP ATP carrier pr
40	253	16.1	329	2	S48269	mitochondrial car
41	252.5	16.0	307	2	S54080	carrier protein YM
42	252.5	16.0	355	2	T09110	envelope protein L
43	252	16.0	339	2	A41677	ADP ATP carrier pr
44	249.5	15.8	702	2	T16533	hypothetical prote
45	247	15.7	320	2	T37603	probable oxaloacet

ALIGNMENTS

RESULT 1
JC5522
uncoupling protein UCP3, mitochondrial - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 21-Jan-2000
C:Accession: JC5522
R:Vidal-Puig, A.; Solanes, G.; Grujic, D.; Flier, J.S.; Lowell, B.B.
Biochem. Biophys. Res. Commun. 235, 79-82, 1997
A:Title: UCP3: An uncoupling protein homologue expressed preferentially and abundan
A:Reference number: JC5522; PMID:97339440; PMID:9196039
A:Accession: JC5522
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-312 <VID>
A:Cross-references: DDBJ:AF001787; NID:G2198812; PIDD:AA051369.1; PID:G2198813
C:Experimental source: skeletal muscle
C:Comment: This protein is an inner mitochondrial membrane transporter which dissip
C:Genetics:
A:Gene: GDB:UCP3
A:Cross-references: GDB:6278985
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C:Keywords: mitochondrion
F:10-106/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F:113-207/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F:214-301/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 72.9%; Score 1149.5; DB 2; Length 312;

Best Local Similarity 72.4%; Pred. No. 2.6e-91; Mismatches 51; Indels 5; Gaps 3;

DB	1	MVGFKATDVPPTATVFLGATACIADITPEPLDTAKYRLQIGESQGPVATASQYR 60		1	MVGFKATDVPPTATVFLGATACIADITPEPLDTAKYRLQIGESQGPVATASQYR 60
DB	1	MVGFKATDVPPTATVFLGATACIADITPEPLDTAKYRLQIGESQGPVATASQYR 59		1	MVGFKATDVPPTATVFLGATACIADITPEPLDTAKYRLQIGESQGPVATASQYR 59
DB	61	GVNCTITMVRTGSPSLNGLVAGIQRQMSRVSRTIGYDVSKQFYT KGEHHSIGSR 119		61	GVNCTITMVRTGSPSLNGLVAGIQRQMSRVSRTIGYDVSKQFYT KGEHHSIGSR 119
DB	60	GVNCTITMVRTGSPSLNGLVAGIQRQMSRVSRTIGYDVSKQFYT KGEHHSIGSR 119		60	GVNCTITMVRTGSPSLNGLVAGIQRQMSRVSRTIGYDVSKQFYT KGEHHSIGSR 119
DB	120	ILASTTGALAVVAQPTDVVKVRFQQAQRAQ---GGRYQSTVNAVYKTIAREEGRGIM 176		120	ILASTTGALAVVAQPTDVVKVRFQQAQRAQ---GGRYQSTVNAVYKTIAREEGRGIM 176
DB	120	ILASTTGALAVVAQPTDVVKVRFQQAQRAQ---GGRYQSTVNAVYKTIAREEGRGIM 179		120	ILASTTGALAVVAQPTDVVKVRFQQAQRAQ---GGRYQSTVNAVYKTIAREEGRGIM 179
DB	177	KGTSPPNARNAIVNCAELVYTDIKDALIKANIMDDLPCHTSAFAGFCCTVVASPVD 236		177	KGTSPPNARNAIVNCAELVYTDIKDALIKANIMDDLPCHTSAFAGFCCTVVASPVD 236
DB	180	KGTLPIINRINAIVNCAELVYTDIKDALIKANIMDDLPCHTSAFAGFCCTVVASPVD 239		180	KGTLPIINRINAIVNCAELVYTDIKDALIKANIMDDLPCHTSAFAGFCCTVVASPVD 239
DB	237	VVKRRVNSALGOYSSAGHATMLQKGPRAFYKGFMSFRLGSMNVVFVTEQLKR 296		237	VVKRRVNSALGOYSSAGHATMLQKGPRAFYKGFMSFRLGSMNVVFVTEQLKR 296
DB	240	VVKRRVNSALGOYSSAGHATMLQKGPRAFYKGFMSFRLGSMNVVFVTEQLKR 299		240	VVKRRVNSALGOYSSAGHATMLQKGPRAFYKGFMSFRLGSMNVVFVTEQLKR 299
DB	297	ALMAACTSREAPF 309		297	ALMAACTSREAPF 309

Db 300 ALMKVQMLRESPP 312

RESULT 2

A24446
uncoupling protein - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 18-Feb-2000
C/Accession: A32446
R/Balogh, A.G.; Ridley, R.G.; Patel, H.V.; Freeman, K.B.
Biochem. Biophys. Res. Commun. 161, 156-161, 1989
A/Title: Rabbit brown adipose tissue uncoupling protein mRNA: use of only one of two pol
A/Reference number: A32446; MUID:89273628; PMID:2730654
A/Accession: A32446
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-306 <BA>
A/Cross-references: GB:X14696
C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C/Keywords: duplication; mitochondrion; transmembrane protein
F/10-103/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F/109-201/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F/208-295/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 60.9%; Score 959.5; DB 2; Length 306;
Best Local Similarity 61.3%; Pred. No. 5.7e-75;
Matches 164; Conservative 48; Mismatches 63; Indels 5; Gaps 3;

QY 1 MYGKATDVPTATVYKFLGAGTACIADITFPPLDTAKVRLQIQSGSQPVATASQYR 60
DB 1 MYGTTTVDVPTMGVKIFSAVACIADITFPPLDTAKVRLQIQSGSQPVATASQYR 56
QY 61 GVMGTLTMVTEGPRSLVNGVAGLQROMSFASVRLGYDSVQYFTKSEHASISRL 120
DB 57 GVLGTTTLAKTEGPKLISGLPAGLQROISFASRLGYDVTVEFTSGSEFTSLGSKI 116
QY 121 LAGSTGALAVAAQPTDVYKRFQAPARAGGR-RYOSTVNAKYTIAREGFRGLMKG 179
DB 117 SAGLTGGAVALFGLQTEVYKRLQAGSHLGLKPRYGTYNAYRIATSELSLTMKG 176
QY 180 SRVAVANALVNCALVTVYLLIKDALIKANLMTDDPCFHTSAFGAFCFTVYASPVYV 239
DB 177 TPLNLNRVITINCELVTVYLLMGKALVNRHLLADVDPCHLISALVAGFTTLLSPVDV 236
QY 240 TRYVNSALGOYSAGHCALTMLOKGPRAFYKGFPSFLRLGSNNVVMFYVYEQIKRL 299
DB 237 TRFINSIPGQYSPVPCAMTWYKSGPAFFKGFPSFLRLGSNNVVMFYVYEQIKRL 296

RESULT 3

A26294
uncoupling protein - rat
N/Alternate names: UCP
C/Species: Rattus norvegicus (Norway rat)
C/Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Feb-2000
C/Accession: A26294; A29278; S03842; A61566
R/Bouillaud, F.; Weissbach, U.; Ricquier, D.
J. Biol. Chem. 261, 1487-1490, 1986
A/Reference number: A26294; MUID:86111804; PMID:3753702
A/Accession: A26294
A/Molecule type: mRNA
A/Residues: 1-307 <BO>
A/Cross-references: GB:M1814; NID:9207556; PIDN:AA19671.1; PID:9207557
R/Ridley, R.G.; Patel, H.V.; Gerber, G.E.; Morton, R.C.; Freeman, K.B.
Nucleic Acids Res. 14, 4025-4035, 1986
A/Title: Complete nucleotide and derived amino acid sequence of cDNA encoding the mitoch
A/Reference number: A29278; MUID:86232540; PMID:3012461
A/Accession: A29278
A/Molecule type: mRNA
A/Residues: 1-307 <RI2>
A/Cross-references: GB:X03894; GB:M15500; NID:957446; PIDN:CAA27531.1; PID:957447
R/Bouillaud, F.; Raimbault, S.; Ricquier, D.
Biochem. Biophys. Res. Commun. 157, 783-792, 1988

A/Title: The gene for rat uncoupling protein: complete sequence, structure of prime
A/Reference number: S03842; MUID:89076317; PMID:3202878
A/Accession: S03842
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-307 <BO2>

A/Cross-references: EMBL:X12925; NID:957444; PIDN:CAA31392.1; PID:957445
R/Ridley, R.G.; Patel, H.V.; Partlett, C.L.D.; Olynik, K.A.; Reichling, S.; Freeman,
Biochim. Biophys. Res. Commun. 161, 156-161, 1989
A/Title: Immunological detection of cDNA clones encoding the uncoupling protein of
A/Reference number: A61566; MUID:86188126; PMID:2421800
A/Accession: A61566
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 254-307 <RID>
A/Comment: The source of this protein was brown adipocyte mitochondria.
C/Genetics:
A/Introns: 42/3; 109/1; 176/1; 210/1; 270/2
C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C/Keywords: duplication; mitochondrion; transmembrane protein
F/10-103/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F/209-296/Domain: ADP/ATP carrier protein repeat homology <ACPI>

Query Match 58.9%; Score 928.5; DB 2; Length 307;
Best Local Similarity 58.2%; Pred. No. 2.6e-72;
Matches 181; Conservative 52; Mismatches 67; Indels 11; Gaps 4;

QY 1 MYGKATDVPTATVYKFLGAGTACIADITFPPLDTAKVRLQIQSGSQPVATASQYR 60
DB 1 MYGTTTVDVPTMGVKIFSAVACIADITFPPLDTAKVRLQIQSGSQPVATASQYR 56
QY 61 GVMGTLTMVTEGPRSLVNGVAGLQROMSFASVRLGYDSVQYFTKSEHASISRL 119
DB 57 GVLGTTTLAKTEGPKLISGLPAGLQROISFASRLGYDVTVEFTSGSEFTSLGSKI 116
QY 120 LLAGSTGALAVAAQPTDVYKRFQAPARAGGR-RYOSTVNAKYTIAREGFRGLMKG 178
DB 117 ISAGLTGGAVALFGLQTEVYKRLQAGSHLGLKPRYGTYNAYRIATSELSLTMKG 176
QY 179 TSPVAVANALVNCALVTVYLLIKDALIKANLMTDDPCFHTSAFGAFCFTVYASPVYV 238
DB 177 TPLNLNRVITINCELVTVYLLMGKALVNRHLLADVDPCHLISALVAGFTTLLSPVDV 236
QY 239 KTRYVNSALGOYSAGHCALTMLOKGPRAFYKGFPSFLRLGSNNVVMFYVYEQIKRL 298
DB 237 KTRFINSIPGQYSPVPCAMTWYKSGPAFFKGFPSFLRLGSNNVVMFYVYEQIKRL 296
QY 299 MAA-----CTS 304
DB 297 MKSROYVDCTT 307

RESULT 4

S34268
uncoupling protein, inner mitochondrial membrane, brown fat - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Feb-2000
C/Accession: S34268; A24363; S20294; S02427
R/Raimbault, S.; Prieto, S.; Rial, E.; Bouillaud, F.
submitted to the EMBL Data Library, June 1993
A/Reference number: S34268
A/Accession: S34268
A/Molecule type: mRNA
A/Residues: 1-307 <RAI>
A/Cross-references: EMBL:X73138; NID:9312661; PIDN:CAA51653.1; PID:9312662
R/Agulla, H.; Link, T.A.; Klingenberg, K.
EMBO J. 4, 2369-2376, 1985
A/Title: The uncoupling protein from brown fat mitochondria is related to the mito
A/Reference number: A24363; MUID:86081749; PMID:3000775
A/Accession: A24363
A/Molecule type: protein
A/Residues: 2-128; 130-307 <ANU>

A>Note: 128-Phe was also found
 R.Winkler, E.; Klingenberg, M.
 Eur. J. Biochem. 203, 295-304, 1992
 A>Title: Phocoaffinity labeling of the nucleotide-binding site of the uncoupling protein
 A/Reference number: S20294; MUID:92111578; PMID:1730236
 A/Accession: S20294
 A/Molecule type: protein
 A/Residues: 257-307 <MIN>
 R.Bekerskov, C.; Klingenberg, M.
 FEBS Lett. 226, 166-170, 1987
 A>Title: In the uncoupling protein from brown adipose tissue the C-terminus protrudes to
 A/Reference number: S02427; MUID:88083626; PMID:3691813
 A/Accession: S02427
 A/Molecule type: protein
 A/Residues: 300-304 <ECK>
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein
 F/10-103/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F/209-296/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 58.1%; Score 915.5; DB 2; Length 307;
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1 MWGFKATDVPPATVVKFLGAGTACIADLTFFPLDTAKVRLQIGESQGPVATASQYR 60
 1 MNPFTTSEVHPITMGVIFISAGVACIADLTFFPLDTAKVRLQIGESQ----ISSTIRYK 56
 Oy 61 GVGNTITLWRTGEPSSLYNGLVAGLQOMSFASVATGLYDSVKPFTYKSGE-HASISR 119
 Db 57 GVLGTTITLAKTEGLPLVSGLPAGIQRIISFASLITGLYDVQGFESSGKTEPTLNR 116
 Oy 120 LLAGSTTGALAAVAAPDTPVVKRPOARAGGGR-RYOSTVNAKYTIAREEGFRGLMK 178
 Db 117 ISAGMTGVAVAFIQPTBKVYKRLQASHHGKIKRYGTINARIATTESFETLWK 176
 Oy 179 TSPVNAKAIIVNCAELVYDILKDALIKANLMTDDLPCHFTAFAGAGCTTYIASPDVY 238
 Db 177 TTPNLINVLINCELVETVYDLMKGLVNNQIADVPCHILSAFVAGFCTTFILASPDVY 236
 Oy 239 KTRVNSALGOYSAGHCALTMLOKSGRAFYKGFPSFLRLGSMNVVMFVYEQLRAL 298
 Db 237 KTRFINSLPQGYPSVSCAMTMTLKSGPTAFKGFVPSFLRLASNVIMFVCEQLKEL 296
 Oy 299 MAA-----CTS 304
 Db 297 SKSRQIVDCTT 307

RESULT 5

G01858
 uncoupling protein 1, mitochondrial - human
 N/Alternate names: UCP1
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence revision 06-Jun-1997 #text_change 20-Jun-2000
 C/Accession: G01858; S78473; S29141; A60793; A45763
 R/Bouilland, F.
 submitted to the EMBL Data Library, June 1995
 A/Reference number: G08642
 A/Accession: G01858
 A/Status: translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-307 <BOU1>
 A/Cross-References: EMBL:U28480; NID:G1155218; PIDN:AA65271.1; PID:G1155219
 A/Accession: S78473
 A/Molecule type: DNA
 A/Residues: 1-20, 'P', 22-307 <BOU2>
 A/Cross-References: EMBL:X51952; NID:937606; PIDN:CAA6214.1; PID:G1177311
 R/Casard, A.M.; Bouilland, F.; Martel, M.G.; Hentz, E.; Raimbault, S.; Thomas, M.; Ricq
 J. Cell. Biochem. 43, 255-264, 1990
 A>Title: Human uncoupling protein gene: structure, comparison with rat gene, and assignm
 A/Reference number: A45763; MUID:90338166; PMID:2380264

A/Accession: S29141
 A/Molecule type: DNA
 A/Residues: 1-20, 'P', 22-108, 'SK', 111, 113-133, 'S', 135-197, 'T', 199-216, 'U', 218-307 <C
 A/Cross-References: EMBL:X51952; NID:937606; PIDN:CAA6214.1
 R/Bouilland, F.; Villalby, F.; Hentz, E.; Raimbault, S.; Casard, A.M.; Ricquier,
 Clin. Sci. 75, 21-27, 1988
 A>Title: Detection of brown adipose tissue uncoupling protein mRNA in adult patient;
 A/Reference number: A60793; MUID:88311701; PMID:3165741
 A/Accession: A60793
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 113-133, 'S', 135-196 <BOU>
 A/Comment: This protein is responsible for the generation of heat by brown fat.
 C/Genetics:
 A/Genes: GDB:UCP1; UCP
 A/Cross-References: GDB:128179; OMIM:113730
 A/Map position: 4q31-4q31
 A/Intons: 42/3, 109/1, 176/1, 210/1, 270/2
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: adipose tissue; duplication; mitochondrion; transmembrane protein
 F/10-103/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F/209-296/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 58.1%; Score 915; DB 2; Length 307;
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 Matches 178; Conservative 48; Mismatches 68; Indels 6; Gaps 3;

1 MWGFKATDVPPATVVKFLGAGTACIADLTFFPLDTAKVRLQIGESQGPVATASQYR 60
 1 MGLTASDVHPTLQGLPSAGIACIADLTFFPLDTAKVRLQIGESQ---TSVIRYK 56
 Db 61 GVGNTITLWRTGEPSSLYNGLVAGLQOMSFASVATGLYDSVKPFTYKSGE-HASISR 119
 Oy 57 GVLGTTITLAKTEGLPLVSGLPAGIQRIISFASLITGLYDVQGFESSGKTEPTLNR 116
 Db 120 LLAGSTTGALAAVAAPDTPVVKRPOARAGGGR-RYOSTVNAKYTIAREEGFRGLMK 178
 Oy 117 ISAGMTGVAVAFIQPTBKVYKRLQASHHGKIKRYGTINARIATTESFETLWK 176
 Db 179 TSPVNAKAIIVNCAELVYDILKDALIKANLMTDDLPCHFTAFAGAGCTTYIASPDVY 238
 Oy 177 TTPNLINVLINCELVETVYDLMKGLVNNQIADVPCHILSAFVAGFCTTFILASPDVY 236
 Db 239 KTRVNSALGOYSAGHCALTMLOKSGRAFYKGFPSFLRLGSMNVVMFVYEQLRAL 298
 Oy 237 KTRFINSLPQGYPSVSCAMTMTLKSGPTAFKGFVPSFLRLASNVIMFVCEQLKEL 296

RESULT 6

A31106
 mitochondrial uncoupling protein - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 21-Jul-2000
 C/Accession: A31106
 R/Kozak, L.P.; Britton, J.H.; Kozak, U.C.; Wells, J.M.
 J. Biol. Chem. 263, 12274-12277, 1988
 A>Title: The mitochondrial uncoupling protein gene. Correlation of exon structure t
 A/Reference number: A31106; MUID:88315014; PMID:3410843
 A/Accession: A31106
 A/Molecule type: DNA; mRNA
 A/Residues: 1-306 <KOZ>
 A/Cross-References: GB:U63418; NID:G1519064; PIDN:AAB07367.1; PID:G1519065
 C/Genetics:
 A/Genes: Ucp
 A/Intons: 41/3, 106/1, 175/1, 209/1, 269/2
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C/Keywords: duplication; mitochondrion; transmembrane protein
 F/9-102/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F/109-201/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F/208-295/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 Query Match 57.8%; Score 911.5; DB 2; Length 306;

Best Local Similarity 58.0%; Pred. No. 7, 6e-71;
Matches 177; Conservative 53; Mismatches 64; Indels 11; Gaps 4;

QY 7 TDVPTATVFKFLGAGTAACIADLTTPPLDTAKVRLQIQESGCPVATASQRYGMGII 66
Db SEVOPFMGVKIFSGVAGSCLADITPPLDTAKVRLQIQESGCPVATASQRYGMGII 61
QY 67 LTMRTGSRSLVNLGLVAGLOROMSPASVRIGLYDSVKQFYTKGSE-HASIGSRLLAGST 125
Db 62 TTKAKTGLPKLISGLPAGIRQISFASLIGLYDSVQEFSSGGRTPSLNKSISAGIM 121
QY 126 TGAALAVAAOPTDVVKVRFQAQARAGGR-RYOSTVNAVYKTAREEGFRGLMKGTSFNVA 184
Db 122 TGVAVAFIIGQPTVEVKVMAQASHLHGIRPYGTAVYAVIATTESLSTLMKGTTPNIM 181
QY 185 RNATVNCALVTVLIDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 244
Db 182 RNATVNCALVTVLIDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 241
QY 245 SALGQSSAGHCALTMLQKGPRAFYKGFMPSPURLGSMNVNMFVTEQIKALMAA--- 301
Db 242 SLPGQYSPVSCAMSMYKKEGPTAFPKGFVASFLRGSNNVIMFVCEQLKMKSRQOT 301
QY 302 --CTS 304
Db 302 VDCCT 306

RESULT 7

uncoupling protein - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Jun-2000

C/Accession: S03603; S05075

C/Keywords: duplication; mitochondrion; transmembrane protein

F.1-87/Domain: ADP, ATP carrier protein repeat homology (fragment) <ACPI>

F.192-184/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F.191-277/Domain: ADP, ATP carrier protein repeat homology <ACP3>

A/Reference number: S03603; MUID:89183626; PMID:12928121

A/Accession: S03603

A/Molecule type: mRNA

A/Residues: 1-288 <CAS>

A/Cross-references: EMBL:X14064; NID:g1495201; PIDN:CAA32227.1; PID:g1495202

R/Ricquier, D.

submitted to the EMBL Data Library, January 1989

A/Reference number: S05075

A/Accession: S05075

A/Molecule type: mRNA

A/Residues: 1-195,201,'T',203,'RCC',204-288 <RIC>

A/Cross-references: EMBL:X14064

C/Suprafamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C/Keywords: duplication; mitochondrion; transmembrane protein

F.1-87/Domain: ADP, ATP carrier protein repeat homology (fragment) <ACPI>

F.192-184/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F.191-277/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 57.6%; Score 907.5; DB 2; Length 288;

Matches 175; Conservative 49; Mismatches 50; Indels 7; Gaps 4;

QY 20 AGTACIADLTTPPLDTAKVRLQIQESGCPVATASQRYGMGII 79
Db 4 AGTACIADLTTPPLDTAKVRLQIQESGCPVATASQRYGMGII 79
QY 80 NGIYAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGSRLLAGSTGALAVAAOPTDV 139
Db 60 SGLPAGIRQISFASLIGLYDSVQEFSSGGRTPSLNKSISAGIM 121
QY 140 VYKRFQAQARAGGR-RYOSTVNAVYKTAREEGFRGLMKGTSFNVA 184
Db 119 VYKRFQAQARAGGR-RYOSTVNAVYKTAREEGFRGLMKGTSFNVA 184
QY 199 LKDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 244
Db 199 LKDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 244

Db 179 LKDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 244
QY 259 TMLQKGPRAFYKGFMPSPURLGSMNVNMFVTEQIKALMAA--- 301
Db 239 TMLQKGPRAFYKGFMPSPURLGSMNVNMFVTEQIKALMAA--- 301

RESULT 8

uncoupling protein (imported) - Arabidopsis thaliana

N/Alternate names: protein F24B22-70

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 03-Nov-2000

C/Accession: T47570; T52023

C/Keywords: H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.

submitted to the Protein Sequence Database, January 2000

A/Reference number: T23016

A/Accession: T47570

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-306 <BLO>

A/Cross-references: EMBL:AL132957

A/Experimental source: cultivar Columbia; BAC clone F24B22

R/Ricquier, M.

submitted to the EMBL Data Library, August 1997

A/Reference number: T25905

A/Accession: T52023

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-306 <LAL>

A/Cross-references: EMBL:AF001264; PIDN:CAA04638.1

C/Genetics:

A/Map position: 3

A/Intons: 26/3; 98/3; 125/1; 169/3; 202/3; 237/3; 263/3; 292/3

A/Note: F24B22-70

C/Suprafamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match

Best Local Similarity 44.0%; Score 693.5; DB 2; Length 306;

Matches 143; Conservative 43; Mismatches 89; Indels 11; Gaps 6;

QY 17 FLGAGTACIADLTTPPLDTAKVRLQIQESGCPVATASQRYGMGII 75
Db 15 FLGAGTACIADLTTPPLDTAKVRLQIQESGCPVATASQRYGMGII 75
QY 76 RSLVNGVAGLOROMSPASVRIGLYDSVKQFYTKGSEHASIGSRLLAGSTGALAVA 132
Db 72 RSLVNGVAGLOROMSPASVRIGLYDSVKQFYTKGSEHASIGSRLLAGSTGALAVA 130
QY 133 VAOPTDVVKVRFQAQAR--AGGRRYOSTVNAVYKTAREEGFRGLMKGTSFNVA 190
Db 131 VAOPTDVVKVRFQAQAR--AGGRRYOSTVNAVYKTAREEGFRGLMKGTSFNVA 190
QY 191 CAELVTVLIDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 244
Db 191 CAELVTVLIDALIKANLMTDDLPCHFTSAFGAGFCTTVIASPVVVKTRVYN 244
QY 251 SSAGHCALTMLQKGPRAFYKGFMPSPURLGSMNVNMFVTEQIKALMAA--- 301
Db 250 SSAGHCALTMLQKGPRAFYKGFMPSPURLGSMNVNMFVTEQIKALMAA--- 301
QY 250 KATIDCFVTKLSDGPMFAFYKGFIPNIGRLGSMNVNMFVTEQIKALMAA--- 301
Db 250 KATIDCFVTKLSDGPMFAFYKGFIPNIGRLGSMNVNMFVTEQIKALMAA--- 301
RESULT 9
uncoupling protein (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C/Accession: T52024
C/Keywords: H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.

Query Match 30.7%; Score 483.5; DB 2; Length 313;
 Best Local Similarity 34.8%; Pred. No. 5.2e-34;
 Matches 106; Conservative 59; Mismatches 117; Indels 23; Gaps 3;

17 FLGAGTACIADLTTPPLDTAKVRLQIQESGCP-----VRATAS 56
 6 FVEGGIASVINGSTHPLDLIKVRLQHGEPSTTVTLRPAALAPNSPAPLETTS 65

57 AQRGVMGTLITMTREPSRLNGVAGLQRMSPFASVIGLYDSVKQFY- KGEHNS 115
 66 VPKVGFISLGINIVKSEGAALFSGVSAATLRQTLYSTTMGYEVLKKNMDDPESKIN 125

116 IGSRLAGSTGALAVAAOPTDVVKVRFQQAAR--AGGRRYOSTVNAKYTIAREEGR 173
 126 LSRKTGAGLVAGGICAAVGNPADVAMRMQADGRPLAQRNRYAGVGDALRSWKGEVLT 185

174 GIMKGTSPNVAARNALVNCALVYTDLIKDALIKRANLMTDDPCHFTSAPGAGCTTVAS 233
 186 SLMRGSALTINRAMIVTAAQLASYPQFEGILENGVNNDELGTHVVASFAAGFVASVSN 245

224 PVDVVKTRVYNSALGQYSAGCHLTMLOKEGPRAFYKGFMPSPFLRGSNNVMEFYTEQ 293
 246 PVDVVKTRVYNSALGQYSAGCHLTMLOKEGPRAFYKGFMPSPFLRGSNNVMEFYTEQ 305

294 LKRAL 298
 306 VRKLL 310

RESULT 13
 DB613
 Hypothetical protein At2g2500 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C/Accession: D84613
 R/Lin: X; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankam, S.E.; Umayam, L.; Tallon, L.;
 Neuse, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: D84613
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1313 <STO>
 A/Cross-references: GB:AE002093; NID:94544443; PIDN:AAD22351.1; GSDB:GN00139
 A/Map position: 2
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 30.2%; Score 475.5; DB 2; Length 313;
 Best Local Similarity 35.9%; Pred. No. 2.5e-33;
 Matches 108; Conservative 57; Mismatches 115; Indels 21; Gaps 4;

17 FLGAGTACIADLTTPPLDTAKVRLQIQES-----QGPVATASAOYRGV 63
 6 FVEGGIASVINGSTHPLDLIKVRLQHGEPSTTVTLRPAALAPNSPAPLETTS 65

64 GTILMTVTEGPRSLNGVAGLQRMSPFASVIGLYDSVKQFY- KGEHNS:IGSRLA 122
 66 VPKVGFISLGINIVKSEGAALFSGVSAATLRQTLYSTTMGYEVLKKNMDDPESKIN 125

123 GSTTGALAVAAOPTDVVKVRFQQAAR--AGGRRYOSTVNAKYTIAREEGRIGKSTS 180
 126 GALAGALGAVGNPADVAMRMQADGRPLAQRNRYAGVGDALRSWKGEVLT 185

181 PNVARNALVNCALVYTDLIKDALIKRANLMTDDPCHFTSAPGAGCTTVASPDVKT 240
 186 LTRNRAVLVYNSALGQYSAGCHLTMLOKEGPRAFYKGFMPSPFLRGSNNVMEFYTEQ 245

241 RYNN-----SALGQYSAGCHLTMLOKEGPRAFYKGFMPSPFLRGSNNVMEFYTEQ 295

DB 246 RYNNMKVAVGAPFYGKAVDCAKTKVKGIMSLYKGFIPVYSRQAPFTVYLFVTEQVK 305
 QY 296 R 296
 DB 306 K 306

RESULT 14
 H86274
 F7A19.22 protein - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
 C/Accession: H86274
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasey, T.H.; Dewar
 ansen, N.F.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Ki
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tai
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: H86274
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-305 <STO>
 A/Cross-references: GB:AE005172; NID:G5080790; PIDN:AAD39300.1; GSDB:GN00141
 C/Genetics:
 A/Map position: 1
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 29.6%; Score 466; DB 2; Length 305;
 Best Local Similarity 34.6%; Pred. No. 1.6e-32;
 Matches 107; Conservative 58; Mismatches 126; Indels 18; Gaps 7;

5 KATDVPPATVYKFLGACTACIADLTTPPLDTAKVRLQIQESGCPVATASAOYR-GVM 63
 5 RVTNEAPICGT-RILALSLMVAASVTFPDLTKTMQLHGS-----GSASGARIGAF 57

64 GTILMTVTEGPRSLNGVAGLQRMSPFASVIGLYDSVK-----QFVKGEHNSIGSR 119
 58 GVSEIARKEGVIGLYGSLPAIRIRLFTYPIRIRIGENKIGLIVSETNNSLSPLATK 117

120 LLAGSTGALAVAAOPTDVVKVRFQQAAR--AGGRRYOSTVNAKYTIAREEGRIGLM 176
 118 ALVGFSGVIAQVAVASPADLVKRMQADGRVLGQGLKPRYSGPTEAFKILQSEGVKGLM 177

177 KGTSPNVAARNALVNCALVYTDLIKDALIKRANLMTDDPCHFTSAPGAGCTTVASPD 236
 178 KGVLENIORALVLMGELACYDAKHVIVDKIAEDNIFVHTLASIMSGLASTLSLCPAD 237

237 VYKTRVYNSALGQ-YSSAGCHLTMLOKEGPRAFYKGFMPSPFLRGSNNVMEFYTEQ 295
 238 VYKTRVYNSALGQ-YSSAGCHLTMLOKEGPRAFYKGFMPSPFLRGSNNVMEFYTEQ 297

296 PALMAACTS 304
 298 --LLAGISS 304

RESULT 15
 T25459
 Hypothetical protein B0432.4 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
 C/Accession: T25459
 R/Henkhaus, J.; Wohlmann, P.
 submitted to the EMBL Data Library, December 1996
 A/Description: The sequence of C. elegans cosmid B0432.
 A/Reference number: Z20038

A:Accession: T25459
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1323 <H2N>
A:Cross-references: EMBL:U80836; PIDN:AA37890.1; GSPDB:GN00020; CESP:B0432.4
A:Experimental source: strain Bristol N2; clone B0432
C:Genetics:
A:Gene: CESP:B0432.4
A:Map position: 2
A:Introns: 20/2; 99/2; 149/1; 254/3; 306/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 28.3%; Score 446.5; DB 2; Length 323;
Best Local Similarity 33.2%; Pred. No. 8.3e-31;
Matches 99; Conservative 54; Mismatches 132; Indels 13; Gaps 3;

QY 15 VKFLGAGTACIADLTTFPLDTAKVELIQGSQSPVRATASAOYRGVWGTLTWRTG 74
DB 11 VKFAPGGTAGMGATLVVQPLDLYKMRQLSG-----TTGKKEYRSSMHALTSIMKNG 63
QY 75 PRSLYNGLVAGLQROMSFASVRIGLYSVKQFYTKGSEHASIGSRILAGSTTGALAVVA 134
DB 64 VFAYVNGLSAGLRQATYTTTRLTGYAFILERFTEKDKPLSFQMKAVLGMTAGIGISFVG 123
QY 135 QPTDVVAVRFOAQR--AGGGRYQSTVNAKTIAREBGRGLMKGTSFNVARNALVNC 192
DB 124 TPAETALIRMTGDRLPVEQRNRYTGVMNLTRITKEBGLTLMRGCTPTVLAMVANA 183
QY 193 ELVITYDLIKDALKANIMTDLPCQHTSAFGAGFCTTVIASPVVYKTRMNSAL---G 248
DB 184 QLATYSAKQALLASGVQDGIQCHFLASWISGLATTIASMPVDIAKRIQSMKVIDGKP 243
QY 249 QYSSAGCALTMLQKGPRAFYKGFMPSEFLGSMNVVMFVYEQKRALMAACTSEE 306
DB 244 EYKNAFDVWGKVIKNBGIFFALMRGFTPYMRIGPHTVLTFTILEQWNAAYFOYVLKRD 301

Search completed: February 4, 2004, 09:19:56
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 09:15:43 ; Search time 41 Seconds

(without alignments)
1944.835 Million cell updates/sec

Title: US-09-884-814-1

Perfect score: 1576

Sequence: 1 MWGFKATDVPPATVTKFLGA.....TYEQIKRALMAACTSRBAPP 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1519	96.4	309	11 Q9R246	Q9R246 mus musculus
2	1502	95.3	309	11 Q8CBUC	Q8CBUC mus musculus
3	1500	95.2	309	11 Q9R17	Q9R17 phodopus su
4	1320	83.8	273	6 Q9X8E1	Q9X8E1 bos taurus
5	1141.5	72.4	299	11 Q9ER16	Q9ER16 phodopus su
6	1114	70.7	307	13 Q9DX50	Q9DX50 meleagris g
7	1109	70.4	307	13 Q9DDT7	Q9DDT7 gallus gall
8	1106	70.2	307	13 Q8AYM4	Q8AYM4 gallus gall
9	1085.5	68.9	304	13 Q8BR90	Q8BR90 eupetomera
10	965	61.2	309	6 Q9GM21	Q9GM21 canis famli
11	901.5	57.2	307	11 Q8K404	Q8K404 dicostonyx
12	899.5	57.1	307	11 Q9ER18	Q9ER18 phodopus su
13	852.5	54.1	224	13 Q8QG96	Q8QG96 pagrus majo
14	745.5	47.3	154	6 Q9N1D9	Q9N1D9 macaca mula
15	695.5	44.1	300	10 Q9AVG1	Q9AVG1 oryza sativ
16	693.5	44.0	306	10 Q81845	Q81845 arabidopsis

17	693	44.0	310	10 Q8S4C4	Q8S4C4 zea mays (m
18	687	43.6	304	10 Q8JNZ1	Q8JNZ1 hellicodicer
19	684.5	43.4	193	6 Q9N1D8	Q9N1D8 macaca mula
20	684.5	43.4	303	10 Q85623	Q85623 arabidopsis
21	674.5	42.8	306	10 Q9MBE7	Q9MBE7 symplocarpu
22	671.5	42.6	306	10 Q24391	Q24391 solanum tub
23	670.5	42.5	306	10 Q8S4S8	Q8S4S8 lycopersico
24	619.5	39.3	305	10 Q9ZMG1	Q9ZMG1 arabidopsis
25	616	39.1	293	10 Q9AVG2	Q9AVG2 oryza sativ
26	601.5	38.2	286	10 Q9FXO5	Q9FXO5 triticum ae
27	594	37.7	268	10 Q9MBE6	Q9MBE6 symplocarpu
28	593.5	37.7	286	10 Q9FXO6	Q9FXO6 triticum ae
29	543.5	34.5	241	10 Q8W1A4	Q8W1A4 glycine max
30	541.5	34.4	242	10 Q94UF6	Q94UF6 mangifera i
31	538	34.1	241	10 Q8W1A3	Q8W1A3 glycine max
32	522	33.1	291	6 Q8HX53	Q8HX53 macaca fasc
33	520.5	33.0	322	11 Q9JMH0	Q9JMH0 rattus norv
34	520.5	33.0	325	11 Q9EP88	Q9EP88 rattus norv
35	520	33.0	291	11 Q9CR58	Q9CR58 mus musculu
36	517.5	32.8	353	11 Q8CU23	Q8CU23 mus musculu
37	517.5	32.8	356	11 Q8CU23	Q8CU23 mus musculu
38	502.5	31.9	155	6 Q9N1E0	Q9N1E0 macaca mula
39	500.5	31.8	141	6 Q9TTL1	Q9TTL1 canis famli
40	495	31.4	340	5 Q9VX14	Q9VX14 drosophila
41	486	30.8	322	11 Q9EPH7	Q9EPH7 rattus norv
42	484.5	30.7	313	10 Q8LDF6	Q8LDF6 arabidopsis
43	483.5	30.7	313	10 Q9S852	Q9S852 arabidopsis
44	479.5	30.4	303	5 Q9TWM8	Q9TWM8 drosophila
45	476	30.2	322	11 Q9D6D0	Q9D6D0 mus musculu

ALIGNMENTS

RESULT 1

Q9R246 PRELIMINARY; PRT: 309 AA.

AC Q9R246; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Uncoupling protein 2.
GN UCP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAST/EI.
RX MEDLINE=99269912; PubMed=1037618;
RA York B., Truett A.A., Monteliro W.P., Barry S.U., Warden C.H.,
RA Naggert J.K., Maddatu T.P., West D.B.;
RT "Gene-environment interaction: a significant diet-dependent obesity
RT locus demonstrated in a conspecific segment on mouse chromosome 7.";
RL Mamm. Genome 10:457-462(1999)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF111999; AAD17199.1; -.
DR MGD; MGI:105354; Ucp2.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr_3.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ Membrane 309 AA; 33313 MW; B09794EBA99810FO CRC64;

Query Match 96.4%; Score 1519; DB 11; Length 309;
Best Local Similarity 96.4%; Pred. No. 6,8e-120;
Matches 298; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

1 MWGFKATDVPPATVTKFLGAGTACACADITPTLTATYARLQIQESGSPFATASAYR 60
|||||

```

Db      1 MVEGKATDVPPATVTKFVLGAGTACIADITLTPFLDTAKVRLQIQSGSGLVRTASAGYR 60
QY      61 GWMGTILTWRTGPRSLYNGVLVAGLQRMSPASVRIGLYDVVKQFYTKGSHASIGSRL 120
Db      61 GVLGTLITWRTGPRSLYNGVLVAGLQRMSPASVRIGLYDVVKQFYTKGSHASIGSRL 120
QY      121 LAGSTGALAVAAQPTDVVKVRFQQAARAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
Db      121 LAGSTGALAVAAQPTDVVKVRFQQAARAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
QY      181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
Db      181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
QY      241 RYNNASALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLGSMNVVMFVTEQLKRALMA 300
Db      241 RYNNASALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLGSMNVVMFVTEQLKRALMA 300
QY      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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RESULT 2

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Q8CBU0 ID PRELIMINARY; PRT; 309 AA.
Q8CBU0 ID
AC 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Uncoupling protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK035298; BAC29021.1;
SQ SEQUENCE 309 AA; 33388 MW; 6E6454DAC14D99DE CRC64;

```

Query Match 95.3%; Score 1502; DB 11; Length 309;

Best Local Similarity 95.8%; Pred. No. 1.8e-118;

Matches 296; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

```

QY      1 MVEGKATDVPPATVTKFVLGAGTACIADITLTPFLDTAKVRLQIQSGSGLVRTASAGYR 60
Db      1 MVEGKATDVPPATVTKFVLGAGTACIADITLTPFLDTAKVRLQIQSGSGLVRTASAGYR 60
QY      61 GWMGTILTWRTGPRSLYNGVLVAGLQRMSPASVRIGLYDVVKQFYTKGSHASIGSRL 120
Db      61 GVLGTLITWRTGPRSLYNGVLVAGLQRMSPASVRIGLYDVVKQFYTKGSHASIGSRL 120
QY      121 LAGSTGALAVAAQPTDVVKVRFQQAARAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
Db      121 LAGSTGALAVAAQPTDVVKVRFQQAARAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
QY      181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
Db      181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
QY      241 RYNNASALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLGSMNVVMFVTEQLKRALMA 300
Db      241 RYNNASALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLGSMNVVMFVTEQLKRALMA 300
QY      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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Db 301 AYESREAPF 309

RESULT 3

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Q9ER17 ID PRELIMINARY; PRT; 309 AA.
Q9ER17 ID
AC 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Uncoupling protein 2.
OS Podopus surinensis (Striped hairy-footed hamster) (Djungarian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Podopus.
OX NCBI_TaxId=10044;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA von Praun C.; Burkert M.; Gessner M.; Klingenspor M.;
RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling
RT proteins in the Djungarian hamster."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF271264; AAC33984.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR Pfam; PF00153; mltc_carr; 3.
DR PRINTS; PR00784; MITOCH_CARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 309 AA; 33359 MW; 9D9C4C1B169F2771 CRC64;

```

Query Match 95.2%; Score 1500; DB 11; Length 309;

Best Local Similarity 95.1%; Pred. No. 2.7e-118;

Matches 294; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

QY      1 MVEGKATDVPPATVTKFVLGAGTACIADITLTPFLDTAKVRLQIQSGSGLVRTASAGYR 60
Db      1 MVEGKATDVPPATVTKFVLGAGTACIADITLTPFLDTAKVRLQIQSGSGLVRTASAGYR 60
QY      61 GWMGTILTWRTGPRSLYNGVLVAGLQRMSPASVRIGLYDVVKQFYTKGSHASIGSRL 120
Db      61 GVLGTLITWRTGPRSLYNGVLVAGLQRMSPASVRIGLYDVVKQFYTKGSHASIGSRL 120
QY      121 LAGSTGALAVAAQPTDVVKVRFQQAARAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
Db      121 LAGSTGALAVAAQPTDVVKVRFQQAARAGGRRYQSTVEAKTIAEEGIRGLMKGTS 180
QY      181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
Db      181 PNVARNAIVNCALVETVDLIKDALIKANIMTDDLPCHFTSAFGAGCTTVIASPVDVYKT 240
QY      241 RYNNASALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLGSMNVVMFVTEQLKRALMA 300
Db      241 RYNNASALGOYSSAGHCALTMLOKEGPRAFYKGFMPSEFLGSMNVVMFVTEQLKRALMA 300
QY      301 ACTSREAPF 309
Db      301 ACTSREAPF 309

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RESULT 4

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Q9XSEL ID PRELIMINARY; PRT; 273 AA.
Q9XSEL ID
AC 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Uncoupling protein 2 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
 RN NCBI_TaxID=9913;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Stone R.T., Rexroad C.E., Smith T.P.L.;
 RT "Bovine UCP2 and UCP3 map to BTA15";
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF127029; AAD29572.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carri_3.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 2.
 FT NON TER 1
 SO SEQUENCE 273 AA; 29638 MW; 40DAF6CB47AAB48 CRC64;

Query Match 83.8%; Score 1320; DB 6; Length 273;
 Best Local Similarity 94.9%; Pred. No. 3,4e-103;
 Matches 259; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 37 AKVRLQIQESQGPVATASQYAGVMTGLITVWTEGPRSLYNGLVAGLQROMSFASVR 96
 DB 1 AKVRLQIQESQGPVATASQYAGVMTGLITVWTEGPRSLYNGLVAGLQROMSFASVR 60
 QY 97 IGLYDVAKQFTTKSEHASISGSLLAGSTTGALAVVAOPTDVYKVRFOAQRAGGRRY 156
 DB 61 IGLYDVAKQFTTKSEHASISGSLLAGSTTGALAVVAOPTDVYKVRFOAQRAGGRRY 120
 QY 157 QSTVAVYKTIARESGPRGLWKTSPVARNALVNCALVLYDILKALKNLMTDDLPC 216
 DB 121 QSTVAVYKTIARESGPRGLWKTSPVARNALVNCALVLYDILKALKNLMTDDLPC 180
 QY 217 HFTSAFAGGCTTCTTASPVYVYKRYNSALGQYSSAGHCAITMLCKEGRPAFYGFMP 276
 DB 161 HFTSAFAGGCTTCTTASPVYVYKRYNSALGQYSSAGHCAITMLCKEGRPAFYGFMP 240
 QY 277 FLRLGSNNVVFVTEQKRALNMACTREAPF 309
 DB 241 FLRLGSNNVVFVTEQKRALNMACTREAPF 273

RESULT 5

QSER16 PRELIMINARY; PRT; 299 AA.
 ID QSER16
 AC QSER16;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Uncoupling protein 3 (Fragment).
 OS Photopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Photopus.
 NCBI_TaxID=10044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Brown adipose tissue;
 RA von Praun C., Burkert M., Gesener M., Klingenspor M.;
 RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling
 RT proteins in the Djungarian hamster";
 RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF271265; AAG33985.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR Pfam; PF00153; mito_carri_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 FT NON TER 299
 SO SEQUENCE 299 AA; 32784 MW; AB5C947B4DDC49A0 CRC64;

Query Match 72.4%; Score 1141.5; DB 11; Length 299;
 Best Local Similarity 73.4%; Pred. No. 4,2e-88;
 Matches 221; Conservative 33; Mismatches 40; Indels 7; Gaps 3;

QY 1 MYGFRATDVPPATVYKFLGAGTACIADLTTPUDTKVRLQIQESQGPVATASQYR 60
 DB 1 MYGFRATDVPPATVYKFLGAGTACIADLTTPUDTKVRLQIQESQGPVATASQYR 56
 QY 61 GVMGTLITVWTEGPRSLYNGLVAGLQROMSFASVRIGLYDVAKQFTT-KSEHASISGR 119
 DB 57 GVMGTLITVWTEGPRSLYNGLVAGLQROMSFASVRIGLYDVAKQFTT-KSEHASISGR 116
 QY 120 LLAGSTTGALAVVAOPTDVYKVRFOAQR--AGGGRYQSTVAVYKTIARESGPRGLW 177
 DB 117 LLAGSTTGAMVTCQPTDVYKVRFOAMITLQGERKXKCTMDAYRTIARESGRGLMK 176
 QY 178 GTSPPVARNALVNCALVLYDILKALKNLMTDDLPCFTSAPFAGCTTIVASPVY 237
 DB 177 GTSPPVARNALVNCALVLYDILKALKNLMTDDLPCFTSAPFAGCTTIVASPVY 236
 QY 238 VTRVYNSALGQYSSAGHCAITMLCKEGRPAFYGFMPFLRGSNNVVFVTEQKRA 297
 DB 237 VTRVYNSALGQYSSAGHCAITMLCKEGRPAFYGFMPFLRGSNNVVFVTEQKRA 296
 QY 298 L 298
 DB 297 L 297

RESULT 6

Q90X50 PRELIMINARY; PRT; 307 AA.
 ID Q90X50
 AC Q90X50;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Uncoupling protein UCP.
 OS Melospiza gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archaeopteryx; Aves; Neognathae; Galliformes; Meleagrididae; Meleagrids.
 NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Skeletal muscle;
 RA Ewok-Clover C.M., Pech S.M., Richards M.P.;
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF436811; AAL28138.1;
 DR InterPro; IPR000794; ketocyl-synt.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR002030; Mit_uncoupling.
 DR InterPro; IPR001950; TIF_SUI1.
 DR Pfam; PF00153; mito_carri_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTNCOUPLING.
 DR PROSITE; PS00606; B_KETOACCT_SYNTHASE; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS01118; SUI1; 1.
 SO SEQUENCE 307 AA; 33148 MW; 256566D6B82ECCC CRC64;

Query Match 70.7%; Score 1114; DB 13; Length 307;
 Best Local Similarity 71.0%; Pred. No. 9,1e-86;
 Matches 220; Conservative 34; Mismatches 50; Indels 6; Gaps 4;

QY 1 MYGFRATDVPPATVYKFLGAGTACIADLTTPUDTKVRLQIQESQGPVATASQYR 60
 DB 1 MYGFRATDVPPATVYKFLGAGTACIADLTTPUDTKVRLQIQESQGPVATASQYR 59
 QY 61 GVMGTLITVWTEGPRSLYNGLVAGLQROMSFASVRIGLYDVAKQFTT-KSEHASISGR 119
 DB 60 GVMGTLITVWTEGPRSLYNGLVAGLQROMSFASVRIGLYDVAKQFTT-KSEHASISGR 119

QY 120 LLAGSTTGALAAVAOPTDVVKRFOA-QAPAGGGRYOSTVNAKYTTIAREEGFRGLMKG 178
 DB 120 LLAGCTGAAVAATCAOPTDVVKRFOALGALPESNRKRYSGVAVAFRIAREEGFRGLMKG 179
 QY 179 TSPNVARNAIVNCAELVYDILIKALLKANIMTDDLPCHEFTSAFGAGFCTTVIASPVDVY 238
 DB 180 TLPNTARNIIINGELVYDILIKOTLLRAQIMTDNVCHPFAAFAGFCATVVASPVDVY 239
 QY 239 KTRYNMNSALGOYSSAGHCAITMLQEGEPRAFYKGMPSFLRIGSMNVVMFVTEYEQLRAL 298
 DB 240 KTRYNMNSALGOYRNVPSCILALIMODGISGLYKGFVPSFLRIGSMNVVMFISYEQLOQRYV 299
 QY 299 MAACTSREAP 308
 DB 300 MLA---RSAP 306

RESULT 7

Q9DDT7 PRELIMINARY; PRT: 307 AA.
 AC Q9DDT7
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Mitochondrial uncoupling protein.
 GN UCP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=21092869; PubMed=11171038;
 RA Raimbault S., Dridi S., Denjean F., Lachner J., Couplan E.,
 RA Bouillaud E., Bordes A., Duchamp C., Taouis M., Ricquier D.
 RT "An uncoupling protein homolog putatively involved in facultative
 RT muscle thermogenesis in birds".
 RL Biochem. J. 353:441-444 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood.
 RA Zhao J., Wang Q., Meng H., Gu Z., Li H.
 RT "Cloning and Sequencing of Uncoupling Protein Gene in Chicken".
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF287144; AAC48942.1; -
 DR EMBL: AF433170; ALJ5325.2; -
 DR InterPro: IPR000794; KETOACYL-SYNT.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002087; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001950; TIF_SUII.
 DR Pfam: PF00153; mito_cartr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUOCOUPLING.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR PROSITE: PS01118; SUII_1; 1.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 307 AA; 33130 MW; 33AC1CD66FC1A9CD CRC64;
 SQ
 Query Match 70.4%; Score 1109; DB 13; Length 307;
 Best Local Similarity 70.6%; Pred. No. 2.4e-85;
 Matches 219; Conservative 35; Mismatches 50; Indels 6; Gaps 4;
 QY 1 MVGFKATDVPPATATKFLGAGTAACIADLITFPDLDTAKVRLQIGESQGPVATASQYR 60
 DB 1 MVGLKPEVPPATATKFLGAGTAACIADLITFPDLDTAKVRLQIGESQGPVATASQYR 59
 QY 61 GVGITLTWRTGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
 DB 61 GVGITLTWRTGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119

DB 60 GVLGTSLTWRTGPRSLYNGLVAGLQROMSFASIRIGLYDSVKQLYTPKGAESTGLLAR 119
 QY 120 LLAGSTTGALAAVAOPTDVVKRFOA-QAPAGGGRYOSTVNAKYTTIAREEGFRGLMKG 178
 DB 120 LLAGCTGAAVAATCAOPTDVVKRFOALGALPESNRKRYSGVAVAFRIAREEGFRGLMKG 179
 QY 179 TSPNVARNAIVNCAELVYDILIKALLKANIMTDDLPCHEFTSAFGAGFCTTVIASPVDVY 238
 DB 180 TLPNTARNIIINGELVYDILIKOTLLRAQIMTDNVCHPFAAFAGFCATVVASPVDVY 239
 QY 239 KTRYNMNSALGOYSSAGHCAITMLQEGEPRAFYKGMPSFLRIGSMNVVMFVTEYEQLRAL 298
 DB 240 KTRYNMNSALGOYRNVPSCILALIMODGISGLYKGFVPSFLRIGSMNVVMFISYEQLOQRYV 299
 QY 299 MAACTSREAP 308
 DB 300 MLA---RSAP 306

RESULT 8

Q8AYM4 PRELIMINARY; PRT: 307 AA.
 AC Q8AYM4
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Uncoupling protein.
 GN AVUCP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
 RT and ANT mRNA in chicken skeletal muscle".
 RL FEBS Lett. 0:0-0(2002).
 DR EMBL: AB088685; BAB15532.1; -
 DR EMBL: AB088685; BAB15532.1; -
 SQ SEQUENCE 307 AA; 33116 MW; 33AC1CD66FC1A888 CRC64;
 SQ

Query Match 70.2%; Score 1106; DB 13; Length 307;
 Best Local Similarity 70.3%; Pred. No. 4.3e-85;
 Matches 218; Conservative 36; Mismatches 50; Indels 6; Gaps 4;
 QY 1 MVGFKATDVPPATATKFLGAGTAACIADLITFPDLDTAKVRLQIGESQGPVATASQYR 60
 DB 1 MVGLKPEVPPATATKFLGAGTAACIADLITFPDLDTAKVRLQIGESQGPVATASQYR 59
 QY 61 GVGITLTWRTGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
 DB 61 GVGITLTWRTGPRSLYNGLVAGLQROMSFASVRIGLYDSVKQFYT-KGSEHASIGSR 119
 QY 120 LLAGSTTGALAAVAOPTDVVKRFOA-QAPAGGGRYOSTVNAKYTTIAREEGFRGLMKG 178
 DB 120 LLAGCTGAAVAATCAOPTDVVKRFOALGALPESNRKRYSGVAVAFRIAREEGFRGLMKG 179
 QY 179 TSPNVARNAIVNCAELVYDILIKALLKANIMTDDLPCHEFTSAFGAGFCTTVIASPVDVY 238
 DB 180 TLPNTARNIIINGELVYDILIKOTLLRAQIMTDNVCHPFAAFAGFCATVVASPVDVY 239
 QY 239 KTRYNMNSALGOYSSAGHCAITMLQEGEPRAFYKGMPSFLRIGSMNVVMFVTEYEQLRAL 298
 DB 240 KTRYNMNSALGOYRNVPSCILALIMODGISGLYKGFVPSFLRIGSMNVVMFISYEQLOQRYV 299
 QY 299 MAACTSREAP 308
 DB 300 MLA---RSAP 306
 RESULT 9
 Q98T90

ID Q98790 PRELIMINARY; PRT; 304 AA.
 AC Q98790;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DT Mitochondrial uncoupling protein UCP.
 OS Eupomema macroura (swallow-tailed hummingbird).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Aves; Neognathae; Trochiliformes; Trochilidae;
 OC Eupomema.
 NC NCB1_TaxID=153633;
 RX NCB1_TaxID=153633;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Vienna C.R., Hagen T., Zhang C.-Y., Bachman E., Boss O., Gereben B.,
 RA Miescov A.S., Lowell J.B., Biscudo J.E.P.W., Bianco A.C.;
 RT "Cloning and functional characterization of an uncoupling protein
 homolog in hummingbirds";
 RL Physiol. Genomics (Online) 0:0-0(2001).
 CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AF555729; AAK16829.1; -
 DR InterPro; IPR000794; Kctocyl-synt.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR InterPro; IPR001950; TIF_SUIT.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS01118; SUIL_1; 1.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 304 AA; 32833 MW; 3016453B21486795 CRC64;

Query Match 68.9%; Score 1085.5; DB 13; Length 304;
 Best Local Similarity 69.3%; Pred. No. 2,3e-83;
 Matches 210; Conservative 36; Mismatches 54; Indels 3; Gaps 3;

QY 1 MVEGKATDVPPTATVKGAGTACIADLTTFPLDTAKVRLQIGESGQPVATASQYR 60
 DB 1 MVALKSGEMPTAIKRFSGTACFADLTTFPLDTAKVRLQIGESVRLP-RVSGAVER 59
 QY 61 GVMGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLDYSVKQYTT-KSEHASIGR 119
 DB 60 GVLGTLSTMTVBARSRLYRGLAGLQROMSPASIRIGLDYSVKQYTPKGAESTGLAPR 119
 QY 120 LLAGSTGALAANAQPTDVVKVRFQO-APAGGRRYSTVNAKYTIAREGFRGLMK 178
 DB 120 LLAGCTGAANAQPTDVVKVRFQAHGAMPSTRINGTLDAYITIRBSGVGLMRG 179
 QY 179 TSPVANAIVNCAELVYDILKDALKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 238
 DB 180 TLPVANAIVNCELVYDILKDALREHLMADVPCHEFAFGAGCATVAVSPDVY 239
 QY 239 KTRVYNSALGOYSAGHCALMTLOKEGPRAFYKGFMPSEFLRGSNWNVWFVYEOLKRL 298
 DB 240 KTRVYNSAGFGYRNALSCLLALMLQDSITGVYKGFVPSFLRGSNWNVWFICYEOLQRA 299
 QY 299 MAA 301
 DB 300 VLA 302
 RESULT 10
 Q9GMZ1 PRELIMINARY; PRT; 309 AA.
 AC Q9GMZ1;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Uncoupling protein 1 UCP1.
 GN UCP1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCB1_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishida K.;
 RT "Cloning of canine UCPs";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB046106; BAB11684.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 KW SEQUENCE 309 AA; 33279 MW; C4D3352A3B08F1CE CRC64;
 SQ
 Query Match 61.2%; Score 965; DB 6; Length 309;
 Best Local Similarity 62.9%; Pred. No. 3,3e-73;
 Matches 190; Conservative 44; Mismatches 62; Indels 6; Gaps 4;

QY 1 MVEGKATDVPPTATVKGAGTACIADLTTFPLDTAKVRLQIGESGQ-PVATASQY 59
 DB 1 MVRAPSDAPPTLSVRIAAAGACIADMTTFPLDTAKVRLQIGESGQPPRA--PRY 57
 QY 60 RGVNGTILTMVTEGPRSLYNGLVAGLQROMSPASVRIGLDYSVKQYTKG-SHNASIGS 118
 DB 58 RGVLTGVALTARTEGQKLYSGLPAGLQROMSPASIRIGLDYSVREMLSPQGAASLGS 117
 QY 119 LLAGSTGALAANAQPTDVVKVRFQAHGAMPSTRINGTLDAYITIRBSGVGLMRG 177
 DB 118 RISAGVMTGAAVFIQGPTEVVKVRLOASHHGKRPYTYTANVARIATBELTGLMK 177
 QY 178 GTSPPVANAIVNCAELVYDILKDALKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 237
 DB 178 GTTPMLNRVITINCELVYDILKDALKANLMTDDLPCHEFTSAFGAGCTTVIASPDVY 237
 QY 238 VKTRYNSALGOYSAGHCALMTLOKEGPRAFYKGFMPSEFLRGSNWNVWFVYEOLKRA 297
 DB 238 VKTRFVNSVPEQTSVPNCAMTMTKEGPLAFKGFVPSFLRGSNWNVWFVCEOLKRE 297
 QY 298 LM 299
 DB 298 LM 299
 RESULT 11
 Q8K404 PRELIMINARY; PRT; 307 AA.
 AC Q8K404;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Uncoupling protein 1.
 OS Dicrostonyx greenlandicus (northern collared lemming).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
 OC Dicrostonyx.
 NC NCB1_TaxID=85953;
 RX NCB1_TaxID=85953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22069795; PubMed=12075603;
 RA Powell C.S., Blaylock M.L., Wang R., Hunter H.L., Johanning G.L.,
 RA Nagy T.R.;
 RT "Effects of energy expenditure and Ucp1 on photoperiod-induced weight
 gain in collared lemmings";
 RL Obed. Res. 10:541-550(2002).
 DR EMBL; AF515781; AAM49148.1; -
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002030; Mit uncoupling.
 DR Pfam; PF00153; mito_carr_3.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR SEQUENCE 307 AA; 33530 MW; 78D492FD26D4897A CRC64;

Query Match 57.2%; Score 901.5; DB 11; Length 307;
 Best Local Similarity 56.6%; Pred. No. 7.4e-68;
 Matches 177; Conservative 52; Mismatches 71; Indels 11; Gaps 4;

QY 1 MVGKATDVPPATVFKFLGAGTACIADITTPPLDTAKVRLQIGSSGQPVATASQYR 60
 DB 1 MSLITSEVPTMVKVTFSGAGISACIADITTPPLDTAKVRLQIGSSGQ-----TSSTIRX 56
 QY 61 GVMGTLITMVRTEGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQFTYTGSE-HASIGSR 119
 DB 57 GVLGITITLAKTEGMPKLYSGLPAGIQROIISFASIRIGLYDVQVEYFSSGKETPPTLVNR 116
 QY 120 LLAGSTGALAAVAAPQTDVVKVRFQQAARAGGR-RYGSTVAAVYTIAREGFRGLMWG 178
 DB 117 ISAGLMTGVAVFIGQPLEVVKVRLQAQSHHGKRYTQTYNAVRIIATSFSLMWG 176
 QY 179 TSPVARNVAIVNCAELVYTDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIAPVDVY 238
 DB 177 TTPNLMRVVIRNTELVYDLMKGLVNNQIILADVPCHLSALVAGCTTFLASPADVY 236
 QY 239 KTRVNSALGOYSAGHCLTLMQEGPRAFYKGWPSFLRLGSWVVMFVTEQLKRAL 298
 DB 237 KTRFINSLPQYPSVSCAMTMTKEGPTAFKGFVPSFLRLASWVIMFVCEQLKEL 296
 QY 299 MAA-----CTS 304
 DB 297 MMSRQTMDCCT 307

RESULT 12
 QSER18 PRELIMINARY; PRT; 307 AA.
 ID QSER18
 AC 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 1.
 OS Photopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Photopus.
 OC NCBI_Taxid=10044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brown adipose tissue;
 RA von Braun C., Burkert M., Gessner M., Klingenspor M.;
 RT "Tissue-specific expression and cold-induced mRNA levels of uncoupling
 proteins in the Djungarian hamster."
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF271263; AAC33983.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Membrane; Transmembrane; Transport.
 SQ SEQUENCE 307 AA; 33364 MW; 7D9ED05FAB39709B CRC64;

Query Match 57.1%; Score 899.5; DB 11; Length 307;
 Best Local Similarity 56.6%; Pred. No. 1.1e-67;
 Matches 176; Conservative 51; Mismatches 73; Indels 11; Gaps 4;

QY 1 MVGKATDVPPATVFKFLGAGTACIADITTPPLDTAKVRLQIGSSGQPVATASQYR 60
 DB 1 MVSQTTSEVPTMVKVTFSGAGIACIADITTPPLDTAKVRLQIGSSGQ-----TSSTIRX 56
 QY 61 GVMGTLITMVRTEGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQFTYTGSE-HASIGSR 119
 DB 57 GVLGITITLAKTEGMPKLYSGLPAGIQROIISFASIRIGLYDVQVEYFSSGKETPPTLVNR 116
 QY 120 LLAGSTGALAAVAAPQTDVVKVRFQQAARAGGR-RYGSTVAAVYTIAREGFRGLMWG 178

DB 117 ISAGLMTGVAVFIGQPLEVVKVRLQAQSHHGKRYTQTYNAVRIIATSFSLMWG 176
 QY 179 TSPVARNVAIVNCAELVYTDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIAPVDVY 238
 DB 177 TTPNLMRVVIRNTELVYDLMKGLVNNQIILADVPCHLSALVAGCTTFLASPADVY 236
 QY 239 KTRVNSALGOYSAGHCLTLMQEGPRAFYKGWPSFLRLGSWVVMFVTEQLKRAL 298
 DB 237 KTRFINSLPQYPSVSCAMTMTKEGPTAFKGFVPSFLRLASWVIMFVCEQLKEL 296
 QY 299 MAA-----CTS 304
 DB 297 MMSRQTMDCCT 307

RESULT 13
 Q08G96 PRELIMINARY; PRT; 224 AA.
 ID Q08G96
 AC Q08G96;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 2 (Fragment).
 OS Pagrus major (Red sea bream) (Chrysophrys major).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Pagrus.
 OC NCBI_Taxid=143350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Liang X., Ogata H.Y., Oku H.;
 RT "Pagrus major mRNA for uncoupling protein 2."
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF487341; AAL92117.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 224 AA; 24686 MW; B8405F9D5A5B8D7 CRC64;

Query Match 54.1%; Score 852.5; DB 13; Length 224;
 Best Local Similarity 73.2%; Pred. No. 6.5e-64;
 Matches 164; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

QY 59 YRGVAGTILMVRTEGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQFTYTGSEHASIGS 118
 DB 1 YRGVAGTILMVRTEGPRSLYNGVLVAGLQRMSPASVRIGLYDSVKQFTYTGSEHASIGS 118
 QY 119 RLLAGSTGALAAVAAPQTDVVKVRFQQAARAGG-GRYOSTVAAVYTIAREGFRGLMWG 177
 DB 61 RLLAGSTGALAAVAAPQTDVVKVRFQQAARAGG-GRYOSTVAAVYTIAREGFRGLMWG 120
 QY 178 GTSNVARNVAIVNCAELVYTDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIAPVDV 237
 DB 121 GTPNITNALVNTCTELVYDLIKDALIKANIMTDDLPCHEFTSAFGAGCTTVIAPVDV 180
 QY 238 VTRVNSALGOYSAGHCLTLMQEGPRAFYKGWPSFLRLGSWVVMFVTEQLKRAL 281
 DB 181 VTRVNSALGOYSAGHCLTLMQEGPRAFYKGWPSFLRLGSWVVMFVTEQLKRAL 224

RESULT 14
 Q9NID9 PRELIMINARY; PRT; 154 AA.
 ID Q9NID9
 AC Q9NID9;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Uncoupling protein 2 (Fragment).

GN UCP2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RA Thompson G.M., Kelly L.J., Candelore M.R.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF202130; AAF34906.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carrt_2
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 KW Membrane; Transport.
 FT NON_TER 1
 FT NON_TER 154
 SQ SEQUENCE 154 AA; 16218 MW; BA0BEFC240C545EB CRC64;

Query Match 47.3%; Score 745.5; DB 6; Length 154;
 Best Local Similarity 98.1%; Pred. No. 4e-55;
 Matches 152; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 4 FKATDYPPETATVFLGAGTAACIADLTTPLDIAKVRLOIQESOGPYRATASQYRGVM 63
 DB 1 FKATDYPPETATVFLGAGTAACIADLTTPLDIAKVRLOIQESOGPYRATAGAYRGVL 60

QY 64 GTLTWRTGEPGLNGVLVAGLQROMSTASVRIGLYDSVKQFYTKGSEHASIGRLLAG 123
 DB 61 GTLTWRTGEPGLNGVLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHASIGRLLAG 120

QY 124 STTGALAAVAVAOPTDVVKVRFQAPAGGARRYOS 158
 DB 121 STTGALAAVAVAOPTDVVKVRFQAPAGGARRYOS 154

RESULT 15
 Q9AVG1 PRELIMINARY; PRT; 300 AA.
 ID Q9AVG1
 AC Q9AVG1
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Uncoupling protein.
 GN OSCP2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euphorbiaceae; Oryzae; Oryza.
 NCBI_TaxID=4530;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Nipponbare;
 RA Watanabe A., Hirai A.;
 RT "Two uncoupling protein genes are present in rice (Oryza sativa L.), but processing of their pre-mRNAs is defective."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB049998; BAB40658.1; -
 DR Gramene: Q9AVG1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carrt_3.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transport.
 SQ SEQUENCE 300 AA; 31909 MW; A1ACBABS5457C592 CRC64;

Query Match 44.1%; Score 695.5; DB 10; Length 300;
 Best Local Similarity 48.4%; Pred. No. 1.ee-50;
 Matches 138; Conservative 49; Mismatches 87; Indels 11; Gaps 5;

QY 16 KFLGAGTAACIADLTTPLDIAKVRLOIQESOGPYRATASQYRGVMGTLTMRTEGG 75
 DB 15 RFTASAIACFAEVCCTLPDIAKVRLOLQKN---VAADAPKRGILGTAIATABEGA 70

QY 76 RSLYGLVAGLQROMSPASVRIGLYDSVKQFYTKGSEHAS---IGRLLAGSTTGALAVA 132
 DB 71 AALMGIVPGLHRCITVGLRIGLYEVKSPYV-GKHVGDVPLTKKIAAGFTGALAIIS 129

QY 133 VAQPTDVVKRPFQAPAR-AGGGRYOSTVNAKYTIABEGRGLMGCTSPNARNAIYNC 191
 DB 130 IANPTDLVKVRLQAGKLAIPGARAYAGMDAYAKIVRQBPALMTGIGNVARNAIINA 189

QY 192 AELVRYDLIKDALKANLMTDLPCHFTSAFGAGCTTIVASPVYVKTFRYNNASALGOYS 251
 DB 190 AELASYDYQKQITLKPGRKDVVYTHLSGLGAGFVAVCVGSPVDVVKSRMGDS--AYT 247

QY 252 SAGHCALTMLQEGEFAFYKGFMPSPFLRSGSNVVFVYTBQLKR 296
 DB 248 STIDCFVKTLKNDGFLAFYKGFLLPFPALGSMVIMFLTEQYOK 292

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